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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:49:03 ; Search time 29.93 Seconds

(Without alignments)  
111.334 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150

Sequence: 1 THRRLAGLSRSGMVKSNFVPTNWSKAF 30

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq\_032802:\*

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:\*

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13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:\*

14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:\*

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16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:\*

17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:\*

18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:\*

19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:\*

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21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:\*

22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	150	100.0	30	22	AAE09806
2	135.5	90.3	29	22	AAE09805
3	135.5	90.3	36	14	AAE09805
4	135.5	90.3	36	14	AAE09805
5	135.5	90.3	36	14	AAE09805
6	135.5	90.3	36	14	AAE09805
7	135.5	90.3	36	14	AAE09805
8	135.5	90.3	36	14	AAE09805
9	135.5	90.3	36	14	AAE09805
10	135.5	90.3	36	14	AAE09805
11	135.5	90.3	36	14	AAE09805

## ALIGNMENTS

12	135.5	90.3	38	7	AAE09806	Sequence of calcit
13	135.5	90.3	38	22	AAE09806	Calcitonin gene r
14	135.5	90.3	39	7	AAE09806	Sequence of calcit
15	135.5	90.3	72	7	AAE09806	Sequence of calcit
16	132.5	88.3	37	11	AAE09806	Calcitonin gene re
17	132.5	88.3	37	11	AAE09806	Calcitonin gene re
18	131.5	87.7	37	11	AAE09806	Calcitonin gene re
19	131.5	87.7	37	11	AAE09806	Calcitonin gene re
20	128.5	85.7	29	14	AAE09806	9-37 peptide B. S
21	128.5	85.7	30	15	AAE09806	(8-37)-CGRP. Homo
22	128.5	85.7	30	22	AAE09806	Calcitonin gene r
23	128.5	85.7	35	21	AAE09806	Peptide ligand pep
24	128.5	85.7	35	21	AAE09806	Peptide ligand pep
25	128.5	85.7	35	22	AAE09806	Nucleic acid trans
26	128.5	85.7	35	22	AAE09806	Nucleic acid trans
27	128.5	85.7	36	14	AAE09806	Desalanyl [Asu2,7]
28	128.5	85.7	36	14	AAE09806	Desalanyl [Asu2,7]
29	128.5	85.7	37	5	AAE09806	Calcitonin gene re
30	128.5	85.7	37	6	AAE09806	Sequence of human
31	128.5	85.7	37	6	AAE09806	Precursor of human
32	128.5	85.7	37	11	AAE09806	Calcitonin gene re
33	128.5	85.7	37	11	AAE09806	Calcitonin gene re
34	128.5	85.7	37	14	AAE09806	Calcitonin gene re
35	128.5	85.7	37	14	AAE09806	Human alpha-CGRP.
36	128.5	85.7	37	16	AAE09806	Human calcitonin g
37	128.5	85.7	37	18	AAE09806	Human calcitonin g
38	128.5	85.7	37	18	AAE09806	Alpha form of calc
39	128.5	85.7	37	19	AAE09806	Alpha-Calcitonin-g
40	128.5	85.7	37	20	AAE09806	Calcitonin gene re
41	128.5	85.7	37	20	AAE09806	Human calcitonin g
42	128.5	85.7	37	22	AAE09806	Calcitonin gene r
43	128.5	85.7	37	22	AAE09806	Calcitonin gene r
44	128.5	85.7	37	22	AAE09806	Human alpha-calcit
45	128.5	85.7	38	21	AAE09806	Pep 14 used in nuc

RESULT 1	AAE09806	standard; peptide: 30 AA.
ID	AAE09806	
XX	AAE09806	
AC	AAE09806	
XX	29-NOV-2001	(first entry)
DE	Alpha-calcitonin gene related peptide (alpha-CGRP).	
XX	Vasoactive peptide; calcitonin gene related peptide; CGRP.	
KW	CGRP-receptor identification.	
XX	Unidentified.	
OS	Unidentified.	
XX	US6268474-B1.	
PN	31-JUL-2001.	
XX	31-JUL-2001.	
PD	30-APR-1998;	98US-0070504.
XX	30-APR-1998;	98US-0070504.
PF	30-APR-1998;	98US-0070504.
XX	30-APR-1998;	98US-0070504.
PR	(UYCR-) UNIT CREIGHTON.	
XX	Smith DD, Saha S, Abel PW;	
PA	WPI: 2001-564216/63.	
XX	Vasoactive peptides useful for inhibiting calcitonin gene related	
PT	peptide receptor activity -	
XX	Claim 2; Column 2; 24pp: English.	
PS		
XX		

CC The invention relates to antagonists of the vasoactive peptide  
 CC calcitonin gene related peptide (CGRP) and other members of the  
 CC CGRP superfamily. The invention also relates to amino the terminal  
 CC modifications of peptides to improve their ability to bind to a  
 CC member of the CGRP-receptor super-family. CGRP antagonists are  
 CC used for inhibiting CGRP activity which can be used in vitro e.g.  
 CC in assays to identify and/or isolate CGRP receptors or with intact  
 CC cells either in vitro or in vivo to inhibit the effect of CGRP  
 CC binding to its receptor. The present sequence is alpha-CGRP peptide  
 CC (8-37).  
 CC  
 XX  
 SQ Sequence 30 AA;

Query Match 100.0%; Score 150; DB 22; Length 30;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-16;  
 Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 THRLAGLSRSGWKSNEFVPTNVGSKAF 30  
 |||||  
 DB 1 thrlagllsrsgwmkfnfvptnvyskaf 30

RESULT 2  
 AAE09805  
 ID AAE09805 standard; peptide; 29 AA.  
 XX  
 AC AAE09805;  
 XX  
 DT 29-NOV-2001 (first entry)  
 XX  
 DE Beta-calcitonin gene related peptide (beta-CGRP).  
 XX  
 KW Vasoactive peptide; calcitonin gene related peptide; CGRP;  
 KW CGRP-receptor identification.  
 XX  
 OS Unidentified.  
 OS  
 XX US6268474-B1.  
 PN  
 XX 31-JUL-2001.  
 PD  
 XX 30-APR-1998; 98US-0070504.  
 PF  
 XX 30-APR-1998; 98US-0070504.  
 PR  
 XX 30-APR-1998; 98US-0070504.  
 XX  
 PA (UYCR-) UNIV CREIGHTON.  
 PA  
 XX Smith DD, Saha S, Abel PW;  
 PI  
 XX WPI; 2001-564216/63.  
 DR  
 XX  
 PT Vasoactive peptides useful for inhibiting calcitonin gene related  
 PT peptide receptor activity -  
 XX  
 PS Claim 2; Column 2; 24pp; English.  
 PS  
 XX  
 CC The invention relates to antagonists of the vasoactive peptide  
 CC calcitonin gene related peptide (CGRP) and other members of the  
 CC CGRP superfamily. The invention also relates to amino the terminal  
 CC modifications of peptides to improve their ability to bind to a  
 CC member of the CGRP-receptor super-family. CGRP antagonists are  
 CC used for inhibiting CGRP activity which can be used in vitro e.g.  
 CC in assays to identify and/or isolate CGRP receptors or with intact  
 CC cells either in vitro or in vivo to inhibit the effect of CGRP  
 CC binding to its receptor. The present sequence is beta-CGRP peptide  
 CC (8-37).  
 CC  
 XX  
 SQ Sequence 29 AA;

Query Match 90.3%; Score 135.5; DB 22; Length 29;  
 Best Local Similarity 96.7%; Pred. No. 2.5e-14;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWKSNEFVPTNVGSKAF 30  
 |||||  
 DB 1 thrlagllsrsgwmkfnfvptnvyskaf 29

RESULT 3  
 AAR42019  
 ID AAR42019 standard; peptide; 36 AA.  
 XX  
 AC AAR42019;  
 XX  
 DT 08-NOV-1993 (first entry)  
 XX  
 DE Desalanyl-desamino human beta-CGRP.  
 XX  
 KW Human; calcitonin gene related peptide; CGRP; blood pressure;  
 KW regulation; hypertension; surgery; hypotensive anaesthesia;  
 KW cerebrovascular disorders.  
 XX  
 OS Synthetic.  
 OS  
 XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note="Desamino-Cys"  
 FT Disulfide-bond 1..6  
 XX  
 PN W09311787-A.  
 XX  
 PD 24-JUN-1993.  
 XX  
 PF 08-DEC-1992; 92WO-JP01600.  
 XX  
 PR 12-DEC-1991; 91JP-0329065.  
 PR 02-DEC-1992; 92JP-0323445.  
 XX  
 PA (ASAH ) ASAMI KASBI KOGYO KK.  
 PA  
 XX Matsumoto K, Shirai T, Takeda S;  
 PI  
 XX WPI; 1993-213820/26.  
 DR  
 XX  
 PT New hypotensive agent contg. calcitonin gene related peptide -  
 PT useful in regulating blood pressure during surgery  
 XX  
 PS Claim 3; Page 3 and 20; 32pp; Japanese.  
 PS  
 XX  
 CC The sequences given in AAR42018-37 represent derivatives of the human  
 CC alpha and beta calcitonin gene related peptides (CGRP). These  
 CC peptides may be used in a blood pressure regulating agent. This  
 CC agent may be used in the treatment of hypertension during surgery,  
 CC for the regulation of blood pressure, during hypotensive anaesthesia  
 CC and in the treatment of cerebrovascular disorders. The agent is fast  
 CC acting and gives high controllability of blood pressure. See also  
 CC AAR38652-67.  
 CC  
 XX  
 SQ Sequence 36 AA;

Query Match 90.3%; Score 135.5; DB 14; Length 36;  
 Best Local Similarity 96.7%; Pred. No. 3.2e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWKSNEFVPTNVGSKAF 30  
 |||||  
 DB 8 thrlagllsrsgwmkfnfvptnvyskaf 36

RESULT 4  
 AAR42021  
 ID AAR42021 standard; peptide; 36 AA.  
 XX

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AC AAR42021;
XX
XX 08-NOV-1993 (first entry)
XX
DE Desalanyl [Asu2,7] human beta-CGRP.
XX
XX Human; calcitonin gene related peptide; CGRP; blood pressure;
KW regulation; hypertension; surgery; hypotensive anaesthesia;
XX cerebrovascular disorders.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1
FT /note="Desamino-Cys, N-terminally modified by Asu
FT at position 6"
FT Misc-difference 6
FT /label= OTHER
FT /note="Asu, linked to the N-terminal of Cys1"
XX
XX WO9311787-A.
XX
XX PD 24-JUN-1993.
XX
XX PF 08-DEC-1992; 92WO-JP01600.
XX
XX PR 12-DEC-1991; 91JP-0329065.
XX PR 02-DEC-1992; 92JP-0323445.
XX
XX PA (ASAH ) ASAMI KASEI KOGYO KK.
XX
XX PI Matsumoto K, Shirai T, Takeda S;
XX
XX DR WPI; 1993-213820/26.
XX
XX FT New hypotensive agent contg. calcitonin gene related peptide -
XX FT useful in regulating blood pressure during surgery
XX
XX PS Claim 3; Page 3 and 20; 32pp; Japanese.
XX
XX CC The sequences given in AAR42018-37 represent derivatives of the human
XX CC alpha and beta calcitonin gene related peptides (CGRP). These
XX CC peptides may be used in a blood pressure regulating agent. This
XX CC agent may be used in the treatment of hypertension during surgery,
XX CC for the regulation of blood pressure, during hypotensive anaesthesia
XX CC and in the treatment of cerebrovascular disorders. The agent is fast
XX CC acting and gives high controllability of blood pressure. See also
XX CC AAR38662-67.
XX
XX SQ Sequence 36 AA;

Query Match 90.3%; Score 135.5; DB 14; Length 36;
Best Local Similarity 96.7%; Pred. No. 3.2e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRAGLIRSGGMVKSNEVPTNVGSKAF 30
   |||||
   8 thrlagllrsggmksnf-vptnvgsakf 36

RESULT 5
AAP60352
ID AAP60352 standard; Peptide; 37 AA.
XX
XX AAP60352;
AC
XX 08-AUG-1991 (first entry)
XX
XX DE Sequence of calcitonin-gene-related peptide (CGRP) (IV).
XX
XX KW Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.
XX

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OS Homo sapiens.
XX
XX PN EP188400-A.
XX
XX PD 23-JUL-1986.
XX
XX PF 10-JAN-1986; 86EP-0810007.
XX
XX PR 16-JAN-1985; 85CH-0000188.
XX
XX PA (CIBA ) CIBA GEIGY AG.
XX
XX PI Jansz HS, Lips CM, Steenbergh PH, Rink H;
XX
XX DR WPI; 1986-191184/30.
XX DR N-PSDB; AAN60266, AAN60267, AAN60268.
XX
XX PT New calcitonin gene related peptide(s) and peptide amide(s) -
XX PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS
XX PT and hypocalcaemic activity
XX
XX PS Claim 1; Page 85 and 33; 96pp; German.
XX
XX CC The inventors claim calcitonin-gene-related peptides (CGRP) contg.
XX CC the aa sequence in AAP60352 as part of a larger peptide with up to 90
XX CC aa residues, or as the sole aa sequence, their derivs. with amidated
XX CC terminal carboxyl gp. and/ or acylated terminal amino gp., and their
XX CC salts. The cysteine residues can form intra- or inter-molecular
XX CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)
XX CC as a partial sequence of a larger sequence with up to 290
XX CC deoxyneucleotides in a single strand.
XX
XX SQ Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 7; Length 37;
Best Local Similarity 96.7%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRAGLIRSGGMVKSNEVPTNVGSKAF 30
   |||||
   9 thrlagllrsggmksnf-vptnvgsakf 37

RESULT 6
AAR04519
ID AAR04519 standard; peptide; 37 AA.
XX
XX AC AAR04519;
XX
XX DT 18-SEP-1990 (first entry)
XX
XX DE Calcitonin gene related peptide analogue.
XX
XX KW Calcitonin; cerebral blood supply deficiencies;
XX KW subarachnoid haemorrhage; stroke; migraine.
XX
XX OS Synthetic.
XX
XX PN EP367463-A.
XX
XX PD 09-MAY-1990.
XX
XX PF 20-OCT-1989; 89EP-0310859.
XX
XX PR 20-OCT-1988; 88GB-0000877.
XX
XX PA (CELL-) CELLTech LTD.
XX
XX PI Eaton MAM, Beeley NRA, Rose CC;
XX
XX DR WPI; 1990-141386/19.
XX

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PT New analogues of calcitonin gene related peptide -  
 PT selectively increase blood flow in the carotid arteries, useful  
 PT for treating cerebral blood supply deficiencies.

XX Claim 7; Page 11; 19pp; English.

CC Useful in treating cerebral blood supply deficiencies, such as  
 CC cerebral stroke, subarachnoid haemorrhage or migraine. The  
 CC compounds may also be useful in treating cardiac disorders and  
 CC hypertension.

XX Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 11; Length 37;  
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKSNEFVPTNWSKAF 30  
 |||||  
 DB 9 thrlaglsrsgwmvksnf-vptnyskaf 37

# RESULT 7

AA38663 standard; peptide; 37 AA.

AA38663;

08-NOV-1993 (first entry)

Human beta-CGRP.

Human; calcitonin gene related peptide; CGRP; blood pressure;  
 regulation; hypertension; surgery; hypotensive anaesthesia;  
 cerebrovascular disorders.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 2..7

WO9311787-A.

24-JUN-1993.

08-DEC-1992; 92WO-JP01600.

12-DEC-1991; 91JP-0329065.

02-DEC-1992; 92JP-0323445.

(ASAH ) ASAH KASEI KOGYO KK.

Matsumoto K, Shirai T, Takeda S;

WPI; 1993-213820/26.

New hypotensive agent conty. calcitonin gene related peptide -  
 useful in regulating blood pressure during surgery

Claim 2; Page 3; 32pp; Japanese.

This sequence represents the human beta calcitonin gene related  
 peptide (CGRP). This peptide, or derivatives of it, may be used in  
 a blood pressure regulating agent. This agent may be used in the  
 treatment of hypertension during surgery, for the regulation of  
 blood pressure, during hypotensive anaesthesia and in the treatment  
 of cerebrovascular disorders. The agent is fast acting and gives  
 high controllability of blood pressure. See also AAR4018-37.

Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 14; Length 37;  
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKSNEFVPTNWSKAF 30  
 |||||  
 DB 9 thrlaglsrsgwmvksnf-vptnyskaf 37

# RESULT 8

AAW31915 standard; peptide; 37 AA.

AAW31915;

02-APR-1998 (first entry)

Beta form of calcitonin gene-related peptide.

Calcitonin gene-related peptide; beta-CGRP; cardiovascular system;  
 progestin; L-arginine donor; nitric oxide donor; preeclampsia; eclampsia;  
 pregnancy; preterm labour; NG-nitro-L-arginine methyl ester; L-NAME;  
 hypertension.

Homo sapiens.

Key Location/Qualifiers

Disulfide-bond 2..7

Modified-site /note="C-terminal amide"

WO974922-A1.

25-SEP-1997.

18-MAR-1997; 97WO-US04310.

19-MAR-1996; 96US-0619841.

(TEXA ) UNIV TEXAS SYSTEM.

Wimalawansa SJ, Yallampalli C;

WPI; 1997-480159/44.

Composition for treating (pre)eclampsia of pregnancy or preterm  
 labour - comprises calcitonin gene-related peptide or analogue and a  
 progestin and/or nitric oxide donor

Claim 11; Page 22; 38pp; English.

This sequence represents the beta-form of the human calcitonin  
 gene-related peptide (beta-CGRP). The alpha- and beta-CGRP's differ in  
 structure by only three amino acids, and each possesses equal biological  
 activity in the cardiovascular system. This sequence, and alpha-CGRP can  
 be used in the composition of the invention which comprises a  
 therapeutically effective amount of CGRP or CGRP analogue; and (a) a  
 progestin; and/or (b) L-arginine or nitric oxide donor. The composition  
 is specifically used to treat preeclampsia and eclampsia of pregnancy, or  
 preterm labour in a pregnant female mammal. CGRP may also be used to  
 remedy NG-nitro-L-arginine methyl ester (L-NAME) induced hypertension.  
 The amino acid residues of the potential cleavage sites have been  
 modified to inhibit biodegradation of CGRP in vivo (no specific details  
 given).

Sequence 37 AA;

Query Match 90.3%; Score 135.5; DB 18; Length 37;  
 Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGWVKSNEFVPTNWSKAF 30

Db 9 thrlagllsrsgmwnsf-vptnvgskaf 37

RESULT 9  
AA939870  
ID AAY39870 standard; peptide: 37 AA.

AC AAY39870;

DT 03-DEC-1999 (first entry)

DE Calcitonin gene related peptide beta form.

KM Calcitonin gene related peptide; CGRP; beta form; human; angioplasty;  
KM pathological vasospasm; ischaemia; impotence; vasoconstrictor peptide;  
KM blood vessel reocclusion; stent insertion; vascular graft; renal failure;  
therapy.

OS Homo sapiens.

PN US5958877-A.

PD 28-SEP-1999.

PF 18-MAY-1995; 95US-0446929.

PR 18-MAY-1995; 95US-0446929.

PA (WIMA/) WIMALAWANSA S J.

PI Wimalawansa SJ;

DR WPI: 1999-561061/47.

PT Counteracting pathological vasospasms or ischaemia in target arteries

PS and treatment of impotence -  
Disclosure; Column 9-10; 9pp; English.

CC This sequence represents the beta form of human calcitonin gene-related  
CC peptide (CGRP). The invention relates to a method for counteracting  
CC pathological vasospasms or ischaemia in target arteries (coronary,  
CC carotid, and renal arteries) comprising administration of CGRP. The  
CC method is useful for the treatment of impotence and for prevention of  
CC vasospasms induced by vasoconstrictor peptides, particularly during  
CC angioplasty or to prevent reocclusion of blood vessels during and/or  
CC after either angioplasty, stent insertion, or the implantation of a  
CC vascular graft. The method can also be used to treat renal failure. The  
CC effects of CGRP are limited to local vascular area, no systemic effects  
CC are induced, making it safe and effective. The method is less invasive  
CC for treatment of reocclusion compared to intracoronary stents (prior  
CC art).

XX Sequence 37 AA;

XX SQ

Query Match 90.3%; Score 135.5; DB 20; Length 37;  
Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLLSRSGMWNFVPTNNGSKAF 30  
Db 9 thrlagllsrsgmwnsf-vptnvgskaf 37

RESULT 10

ID AAB91062 standard; peptide: 37 AA.

AC AAB91062;

DT 22-JUN-2001 (first entry)

XX Calcitonins gene related peptide (CGRP) SEQ ID NO:236.

KM protection; endogenous therapeutic peptide; peptide; conjugation;  
KM blood component; modification; succinimidyl; maleimido group; amino;  
KM hydroxyl; thiol; hormone; growth factor; neurotransmitter.

OS Homo sapiens.  
OS Synthetic.

PN WO200069900-A2.

PD 23-NOV-2000.

PF 17-MAY-2000; 2000WO-US13576.

PR 17-MAY-1999; 99US-0134406.

PR 10-SEP-1999; 99US-0153406.

PR 15-OCT-1999; 99US-0159783.

PA (CONJ-) CONJUCHEM INC.

PI Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;

DR WPI: 2001-112059/12.

PT Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity

PS Disclosure; Page 267; 733pp; English.

CC The present invention describes a modified therapeutic peptide (I)  
CC comprising a therapeutically active amino acid region (II) and a  
CC reactive group (III) (e.g. succinimidyl and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specifically as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.

XX Sequence 37 AA;

XX SQ

Query Match 90.3%; Score 135.5; DB 22; Length 37;  
Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLLSRSGMWNFVPTNNGSKAF 30  
Db 9 thrlagllsrsgmwnsf-vptnvgskaf 37

RESULT 11

ID AAE09807 standard; peptide: 37 AA.

AC AAE09807;

DT 29-NOV-2001 (first entry)

DE Human beta-calcitonin gene related peptide (beta-CGRP).

KM Human; vasoactive peptide; calcitonin gene related peptide; CGRP;

KW CGRP-receptor identification.  
XX  
XX Homo sapiens.  
XX  
XX US6268474-B1.  
XX  
XX 31-JUL-2001.  
XX  
XX 30-APR-1998; 98US-0070504.  
XX  
XX 30-APR-1998; 98US-0070504.  
XX  
XX 30-APR-1998; 98US-0070504.  
XX  
XX (UYCR-) UNIV CREIGHTON.  
XX  
XX Smith DD, Saha S, Abel FW;  
XX  
XX WPI; 2001-564216/63.  
XX  
XX Vasoactive peptides useful for inhibiting calcitonin gene related  
PT peptide receptor activity -  
XX  
XX  
XX Disclosure; Column 19-20; 24pp; English.  
XX  
XX The invention relates to antagonists of the vasoactive peptide  
CC calcitonin gene related peptide (CGRP) and other members of the  
CC CGRP superfamily. The invention also relates to amino the terminal  
CC modifications of peptides to improve their ability to bind to a  
CC member of the CGRP-receptor super-family. CGRP antagonists are  
CC used for inhibiting CGRP activity which can be used in vitro e.g.  
CC in assays to identify and/or isolate CGRP receptors or with intact  
CC cells either in vitro or in vivo to inhibit the effect of CGRP  
CC binding to its receptor. The present sequence is human beta-CGRP  
CC peptide.  
XX  
XX Sequence 37 AA;  
SQ

Query Match 90.3%; Score 135.5; DB 22; Length 37;  
Best Local Similarity 96.7%; Pred. No. 3.3e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 THRLAGLSRSGMWKSNFVPTNNGSKAF 30  
Db 9 thrlaglsrsgmwksnf-vptnvgskaf 37  
|||||

RESULT 12  
AAP60353  
ID AAP60353 standard; Peptide; 38 AA.  
XX  
XX AAP60353;  
AC  
XX 08-AUG-1991 (first entry)  
DT  
XX  
XX Sequence of calcitonin-gene-related peptide (CGRP11a) (XV).  
DE  
XX  
XX Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.  
KW  
XX  
XX Homo sapiens.  
OS  
XX  
XX Key Location/Qualifiers  
FH Disulfide-bond 2..7  
FT Misc-difference 38  
FT /Label= Tyr-OH  
FT  
XX  
XX EPI88400-A.  
XX  
XX 23-JUL-1986.  
XX  
XX 10-JAN-1986; 86EP-0810007.  
XX  
XX 16-JAN-1985; 85CH-0000188.  
XX

PA (CIBA ) CIBA GEIGY AG.  
XX  
XX Jansz HS, Lips CJM, Steenbergh PH, Rink H;  
XX  
XX WPI; 1986-191184/30.  
XX  
XX  
XX New calcitonin gene related peptide(s) and peptide amide(s) -  
PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS  
PT and hypocalcaemic activity  
XX  
XX Example; Page 58; 96pp; German.  
XX  
XX The inventors claim calcitonin-gene-related peptides (CGRP) contg.  
CC the aa sequence in AAP60352 as part of a larger peptide with up to 90  
CC aa residues, or as the sole aa sequence, their derivs. with amended  
CC terminal carboxyl gp. and/or acylated terminal amino gp.; and their  
CC salts. The cysteine residues can form intra- or inter-molecular  
CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)  
CC as a partial sequence of a larger sequence with up to 290  
CC deoxyneucleotides in a single strand.  
XX  
XX Sequence 38 AA;  
SQ

Query Match 90.3%; Score 135.5; DB 7; Length 38;  
Best Local Similarity 96.7%; Pred. No. 3.4e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
QY 1 THRLAGLSRSGMWKSNFVPTNNGSKAF 30  
Db 9 thrlaglsrsgmwksnf-vptnvgskaf 37  
|||||

RESULT 13  
AAB91075  
ID AAB91075 standard; Peptide; 38 AA.  
XX  
XX AAB91075;  
AC  
XX 22-JUN-2001 (first entry)  
DT  
XX  
XX Calcitonins gene related peptide (CGRP) SEQ ID NO:249.  
DE  
XX  
XX Protection; endogenous therapeutic peptide; peptidase; conjugation;  
KW blood component; modification; succinimidy; maleimido group; amino;  
KW hydroxyl; thiol; hormone; growth factor; neurotransmitter.  
XX  
XX Homo sapiens.  
OS  
XX Synthetic.  
XX  
XX WO200069900-A2.  
XX  
XX 23-NOV-2000.  
XX  
XX 17-MAY-2000; 2000WO-US13576.  
XX  
XX 17-MAY-1999; 99US-0134406.  
XX  
XX 10-SEP-1999; 99US-0153406.  
XX  
XX 15-OCT-1999; 99US-0159783.  
XX  
XX (CONJ-) CONJUCHEM INC.  
XX  
XX Bridon DP, Ezrin AM, Milner PG, Holmes DL, Thibaudau K;  
XX  
XX WPI; 2001-112059/12.  
XX  
XX  
XX Modifying and attaching therapeutic peptides to albumin prevents  
PT peptidase degradation, useful for increasing length of in vivo activity  
XX  
XX Disclosure; Page 272; 73pp; English.  
XX  
XX The present invention describes a modified therapeutic peptide (I)

CC comprising a therapeutically active amino acid region (III) and a  
CC reactive group (II) (e.g. succinimide) and maleimido groups) attached to  
CC a less therapeutically active amino acid region (IV), which covalently  
CC bonds with amino/hydroxyl/thiol groups on blood components to form a  
CC peptide stabilised therapeutic peptide composed of 3-50 amino acids.  
CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth  
CC factors and neurotransmitters, to protect them from peptidase activity  
CC in vivo for the treatment of various disorders. Endogenous therapeutic  
CC peptides are not suitable as drug candidates as they require frequent  
CC administration due to rapid degradation by peptidases in the body.  
CC Modifying and attaching therapeutic peptides to albumin prevents or  
CC reduces the action of peptidases to increase length of activity (half  
CC life) and specificity as bonding to large molecules decreases  
CC intracellular uptake and interference with physiological processes.  
CC AAB90829 to AAB92441 represent peptides which can be used in the  
CC exemplification of the present invention.

Sequence 38 AA.

Query Match 90.3%; Score 135.5; DB 22; Length 38;  
Best Local Similarity 96.7%; Pred. No. 3,4e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30  
|||||  
Db 10 thrIagllsrsgmwksnf-vptnvgsKaf 38

RESULT 14

AAP60354  
ID AAP60354 standard; Peptide: 39 AA.

AC AAP60354;

DT 08-AUG-1991 (first entry)

DE Sequence of calcitonin-gene-related peptide (CGRP) (XVII).

KM Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.

OS Homo sapiens.

XX EP188400-A.

PD 23-JUL-1986.

PF 10-JAN-1986; 86EP-0810007.

PR 16-JAN-1985; 85CH-0000188.

PA (CIBA ) CIBA GEIGY AG.

PI Jansz HS, Lips CJM, Steenbergh PH, Rink H;

DR WPI; 1986-191184/30.

XX N-PSDB; AAN60271.

PT New calcitonin gene related peptide(s) and peptide amide(s) -  
PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS  
PT and hypocalcaemic activity

PS Claim 1; Page 85 and 33; 96pp; German.

CC The inventors claim calcitonin-gene-related peptides (CGRP) contg.  
CC the aa sequence in AAP60352 as part of a larger peptide with up to 90  
CC aa residues, or as the sole aa sequence, their derivs. with amidated  
CC terminal carboxyl gp. and/ or acylated terminal amino gp., and their  
CC salts. The cysteine residues can form intra- or inter-molecular  
CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)  
CC as a partial sequence of a larger sequence with up to 290  
CC deoxynucleotides in a single strand.

SO Sequence 39 AA;

Query Match 90.3%; Score 135.5; DB 7; Length 39;  
Best Local Similarity 96.7%; Pred. No. 3,5e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30  
|||||  
Db 10 thrIagllsrsgmwksnf-vptnvgsKaf 38

RESULT 15

AAP60341  
ID AAP60341 standard; peptide; 72 AA.

AC AAP60341;

DT 08-AUG-1991 (first entry)

DE Sequence of calcitonin-gene-related peptide (CGRP) (II).

KM Vasodilatory; hypocalcaemic; hypotensive; myocardial contractility.

OS Homo sapiens.

XX EP188400-A.

PD 23-JUL-1986.

PF 10-JAN-1986; 86EP-0810007.

PR 16-JAN-1985; 85CH-0000188.

PA (CIBA ) CIBA GEIGY AG.

PI Jansz HS, Lips CJM, Steenbergh PH, Rink H;

DR WPI; 1986-191184/30.

XX N-PSDB; AAN60271.

PT New calcitonin gene related peptide(s) and peptide amide(s) -  
PT with vasodilatory, hypotensive, gastric secretion inhibiting, CNS  
PT and hypocalcaemic activity

PS Disclosure; Page 2; 96pp; German.

CC The inventors claim calcitonin-gene-related peptides (CGRP) contg.  
CC the aa sequence in AAP60352 as part of a larger peptide with up to 90  
CC aa residues, or as the sole aa sequence, their derivs. with amidated  
CC terminal carboxyl gp. and/ or acylated terminal amino gp., and their  
CC salts. The cysteine residues can form intra- or inter-molecular  
CC disulphide bridges. Also claimed are DNA sequences (AAN60266, AAN60268)  
CC as a partial sequence of a larger sequence with up to 290  
CC deoxynucleotides in a single strand.

SO Sequence 72 AA;

Query Match 90.3%; Score 135.5; DB 7; Length 72;  
Best Local Similarity 96.7%; Pred. No. 7,3e-14;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGMWKSNFVPTNVGSKAF 30  
|||||  
Db 35 thrIagllsrsgmwksnf-vptnvgsKaf 63

Search completed: August 26, 2002, 15:51:55

Job time: 172 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:50:28 ; Search time 14.83 Seconds  
(without alignments)

194.382 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150  
Sequence: 1 THRLAGLIRSGGMVKSNEFVPTNVGSKAF 30

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.5	90.3	72	2	I37232
2	135.5	90.3	127	2	A25864
3	128.5	85.7	128	1	TCRHR
4	127.5	85.0	37	2	JH0709
5	123.5	82.3	128	1	TCRTR
6	122.5	81.7	134	2	A44173
7	118.5	79.0	128	2	B44173
8	110.5	73.7	125	1	TCCHRP
9	52	34.7	449	2	A48939
10	51	34.0	474	1	I40059
11	51	34.0	474	2	A13349
12	50.5	33.7	89	2	A33542
13	50.5	33.7	135	2	A56855
14	49.5	33.0	261	2	T04301
15	49	32.7	157	2	A24434
16	49	32.7	516	2	US0083
17	49	32.7	516	2	S33164
18	49	32.7	1029	2	T30852
19	48.5	32.3	93	1	TCRPA
20	48.5	32.3	93	1	C33542
21	48	32.0	428	1	SYCR
22	48	32.0	428	2	D90629
23	48	32.0	428	2	D85480
24	48	32.0	429	2	D70784
25	48	32.0	533	2	F70171
26	48	32.0	875	2	T17382
27	48	32.0	1608	1	WMTMG
28	48	32.0	2021	1	A97859
29	47.5	31.7	89	2	S22344

30	47.5	31.7	385	2	C97277	glycosyltransferase
31	47	31.3	428	2	AE0502	threonine synthase
32	47	31.3	711	2	F65201	phosphoenolpyruvate
33	47	31.3	711	2	D91238	PEP-protein phosph
34	47	31.3	711	2	H86085	PEP-protein phosph
35	47	31.3	995	2	C83203	probable serine pr
36	46	30.7	68	2	G81063	hypothetical prote
37	46	30.7	167	2	E87476	conserved hypothet
38	46	30.7	230	2	G81960	hypothetical inner
39	46	30.7	230	2	B81017	conserved hypothet
40	46	30.7	258	2	I40374	N-acetylglutamate
41	46	30.7	292	2	E90180	conserved hypothet
42	46	30.7	400	2	T19517	hypothetical prote
43	46	30.7	434	2	S62813	MG181 homolog G99
44	46	30.7	849	2	T04242	abdominal segment
45	46	30.7	870	2	AE0208	probable outer mem

#### ALIGNMENTS

RESULT 1

I37232  
calcitonin gene-related peptide 2 - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 06-Sep-1996 #sequence\_revision 06-Sep-1996 #text\_change 16-Jul-1999

C:Accession: I37232

R:Steenbergh, P.H.; Hoppe, J.W.; Zandberg, J.; Lips, C.J.; Jansz, H.S.

FEB8 left 183, 403-407, 1985

A:Title: A second human calcitonin/CGRP gene.

A:Reference number: I37232; MUID:85180007

A:Accession: I37232

A:Molecule type: mRNA

A:Residues: 1-72 <RES>

A:Cross-references: EMBL:X02404; NID:g29933; PIDN:CA26249.1; PID:g825642

C:Superfamily: calcitonin

Query Match 90.3%; Score 135.5; DB 2; Length 72;  
Best Local Similarity 96.7%; Pred. No. 6.2e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLIRSGGMVKSNEFVPTNVGSKAF 30

DB 35 THRLAGLIRSGGMVKSNEFVPTNVGSKAF 63

RESULT 2  
A25864  
calcitonin gene-related peptide beta precursor - human

N:Alternate names: calcitonin gene-related peptide II

C:Species: Homo sapiens (man)

C>Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 29-Aug-1997

C:Accession: A25864; JH0620; E26142; A34565

R:Steenbergh, P.H.; Hoppe, J.W.M.; Zandberg, J.; Visser, A.; Lips, C.J.M.; Jansz,

FEB8 left 209, 97-103, 1986

A:Title: Structure and expression of the human calcitonin/CGRP genes.

A:Reference number: A25864; MUID:87105923

A:Accession: A25864

A:Molecule type: DNA

A:Residues: 1-127 <STR>

R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eto, T.

Biochem. Biophys. Res. Commun. 185, 134-141, 1992

A:Title: Isolation and characterization of peptides which act on rat platelets, from

A:Reference number: JH0618; MUID:92287083

A:Accession: JH0620

A:Molecule type: Protein

A:Residues: 82, 'X', 84-87, 'X', 89-104 <KIT>

A:Experimental source: pheochromocytoma

R:Pettermann, J.B.; Born, W.; Chang, J.Y.; Fischer, J.A.

J Biol. Chem. 262, 542-545, 1987

A:Title: Identification in the human central nervous system, pituitary, and thyroid o

A:Reference number: A92637; MUID:87109142  
 A:Accession: B26142  
 A:Molecule type: protein  
 A:Residues: 82,'X','84-87','X','89-91','X','93-98','X','100-105','X','107-109 <P>  
 R:Wimalawansa, S.J.; Morris, H.R.; Etienne, A.; Blench, I.; Panico, M.; MacIntyre, I.  
 Biochem. Biophys. Res. Commun. 167, 993-1000, 1990  
 A:Title: Isolation, purification and characterization of beta-hCGRP from human spinal cord  
 A:Reference number: A34565; MUID:90211348  
 A:Accession: A34565  
 A:Molecule type: protein  
 A:Residues: 82-86;104-117 <MIM>  
 C:Comment: Calcitonin gene-related peptide II peptide is a potent vasorelaxant.  
 C:Geneids:  
 A:Gene: GDB:CALCB; CALC2  
 A:Cross-references: GDB:120572; OMIM:114160  
 A:Map position: 11p15.2-11p15.1  
 C:Superfamily: calcitonin  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:82-118/Product: calcitonin gene-related peptide beta #status experimental <MAT>  
 F:83-88/Disulfide bonds: #status experimental  
 F:118/Modified site: amidated carboxyl end (Phe) (amide in mature form from following g

Query Match 90.3%; Score 135.5; DB 2; Length 127;  
 Best Local Similarity 96.7%; Pred. No. 1.2e-12;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRAGLSRSGGWKSNFVPTNGSKAF 30  
 |||||  
 DB 90 THRAGLSRSGGWKSNF-VPTNGSKAF 118

RESULT 3  
 TCHUR  
 calcitonin gene-related peptide alpha precursor [validated] - human  
 N:Alternate names: calcitonin gene-related peptide I; CGRP-I  
 C:Species: Homo sapiens (man)  
 C:Date: 30-Sep-1987 #sequence\_revision 02-Jul-1996 #text\_change 08-Dec-2000  
 C:Accession: S07644; A22943; B22716; I5536; J00005; S10813; A26142; JH0619; I52204; I84  
 R:Broad, P.M.; Symes, A.J.; Thakker, R.V.; Craig, R.K.  
 Nucleic Acids Res. 17, 6999-7011, 1989  
 A:Title: Structure and methylation of the human calcitonin/alpha-CGRP gene.  
 A:Reference number: S07643; MUID:89386053  
 A:Accession: S07644  
 A:Molecule type: DNA  
 A:Residues: 1-128 <BRO>  
 A:Cross-references: EMBL:X15943; NID:g29613; PIDN:CAA34070.1; PID:g296638  
 A:Note: The authors translated the codon CAG for residue 19 as Glu  
 R:Jonas, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermod, J.J.; Evans, R.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 1994-1998, 1985  
 A:Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related F  
 A:Reference number: A94030; MUID:85166259  
 A:Accession: A22949  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <JON>  
 A:Cross-references: GB:M12667; NID:g179825; PIDN:AAA51914.1; PID:g179828  
 R:Edbrooke, M.R.; Parker, D.; McVey, J.H.; Riley, J.H.; Sorenson, G.D.; Pettengill, O.S.  
 EMBO J. 4, 713-724, 1985  
 A:Title: Expression of the human calcitonin/CGRP gene in lung and thyroid carcinoma.  
 A:Reference number: A91034; MUID:85230541  
 A:Accession: B22716  
 A:Molecule type: mRNA  
 A:Residues: 'V','50-75','S','76-128 <EDB>  
 R:Steinberg, P.H.; Hoppener, J.W.; Zandberg, J.; Van de Ven, W.J.; Jansz, H.S.; Lips, C.  
 J. Clin. Endocrinol. Metab. 59, 358-360, 1984  
 A:Title: Calcitonin gene related peptide coding sequence is conserved in the human genom  
 A:Reference number: I55336; MUID:84240176  
 A:Accession: I55336  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 77-128 <RES>  
 A:Cross-references: GB:M28637; NID:g180467; PIDN:AAA52012.1; PID:g457134  
 R:Morris, H.R.; Panico, M.; Etienne, T.; Tipples, J.; Gargis, S.I.; MacIntyre, I.

Nature 308, 746-748, 1984  
 A:Title: Isolation and characterization of human calcitonin gene-related peptide.  
 A:Reference number: A93329; MUID:84191466  
 A:Accession: J00005  
 A:Molecule type: protein  
 A:Residues: 83-119 <MOR>  
 A:Note: this peptide was detected in medullary thyroid carcinoma tissue and in plasma  
 R:Zaidi, M.; Brain, S.D.; Tipples, J.R.; di Marzo, V.; Moonja, B.S.; Chambers, T.J.;  
 Biochem. J. 269, 775-780, 1990  
 A:Title: Structure-activity relationship of human calcitonin-gene-related peptide.  
 A:Reference number: S10813; MUID:90358780  
 A:Accession: S10813  
 A:Molecule type: protein  
 A:Residues: 83-99,'X','101-119 <ZAI>  
 R:Pettermann, J.B.; Born, M.; Chang, J.Y.; Fischer, J.A.  
 J. Biol. Chem. 262, 542-545, 1987  
 A:Title: Identification in the human central nervous system, pituitary, and thyroid o  
 A:Reference number: A92637; MUID:87109142  
 A:Accession: A26142  
 A:Molecule type: protein  
 A:Residues: 83-88,'X','90-101','X','103-111','X','113-115','X','117 <P>  
 R:Kitamura, K.; Kangawa, K.; Kawamoto, M.; Ichiki, Y.; Matsuo, H.; Eco, T.  
 Biochem. Biophys. Res. Commun. 185, 134-141, 1992  
 A:Title: Isolation and characterization of peptides which act on rat platelets, from  
 A:Reference number: JH0618; MUID:92287083  
 A:Accession: JH0619  
 A:Molecule type: protein  
 A:Residues: 83,'X','85-88','X','90-108 <KIT>  
 A:Experimental source: pheochromocytoma  
 R:Nelkin, B.D.; Rosenfeld, K.I.; de Bustros, A.; Leong, S.S.; Roos, B.A.; Baylun, S.B  
 Biochem. Biophys. Res. Commun. 123, 648-655, 1984  
 A:Title: Structure and expression of a gene encoding human calcitonin and calcitonin  
 A:Reference number: I52204; MUID:85022523  
 A:Accession: I52204  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 48-119 <RE2>  
 A:Cross-references: GB:K03512; NID:g180465; PIDN:AAA52011.1; PID:g180466  
 R:Craig, R.K.; Riley, J.H.; Edbrooke, M.R.; Broad, P.M.; Foord, S.M.; Al-Kazwini, S.J  
 Biochem. Soc. Symp. 52, 91-105, 1986  
 A:Title: Expression and function of the human calcitonin/alpha-CGRP gene in health an  
 A:Reference number: I39387; MUID:87213363  
 A:Accession: I84508  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 77-128 <RE3>  
 A:Cross-references: GB:M6094; NID:g179798; PIDN:AAA51912.1; PID:g179799  
 C:Comment: This peptide is a potent vasorelaxant.  
 C:Comment: This peptide increases the rate and force of contraction of rat auricles 1  
 C:Geneids:  
 A:Gene: GDB:CALCA; CALC1  
 A:Cross-references: GDB:120571; OMIM:114130  
 A:Map position: 11p15.2-11p15.1  
 A:Introns: 29/2; 76/2  
 C:Superfamily: calcitonin  
 C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide; vasodilator  
 F:83-119/Product: calcitonin gene-related peptide alpha #status experimental <CTR>  
 F:84-89/Disulfide bonds: #status experimental  
 F:119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following

Query Match 85.7%; Score 128.5; DB 1; Length 128;  
 Best Local Similarity 90.0%; Pred. No. 1.3e-11;  
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRAGLSRSGGWKSNFVPTNGSKAF 30  
 |||||  
 DB 91 THRAGLSRSGGWKSNF-VPTNGSKAF 119

RESULT 4  
 JH0709  
 calcitonin gene-related peptide - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)  
 C>Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 08-Dec-1995  
 C:Accession: JH0709  
 R: Miyata, A.; Jiang, L.; Minamino, N.; Arimura, A.  
 Biochem. Biophys. Res. Commun. 187, 1474-1479, 1992  
 A:Title: Identification of calcitonin gene related peptide in ovine hypothalamic extract  
 A:Reference number: JH0709; MUID:93038624  
 A:Accession: JH0709  
 A:Molecule type: protein  
 A:Residues: 1-37 <MT>  
 A:Experimental source: hypothalamus  
 C:Comment: This protein has adenylate cyclase stimulating activity.  
 C:Superfamily: calcitonin  
 C:Keywords: amidated carboxyl end; neuropeptide  
 F:37/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 85.0%; Score 127.5; DB 2; Length 37;  
 Best Local Similarity 90.0%; Pred. No. 4,5e-12;  
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWSNFWPTNVGSKAF 30  
 |||||  
 Db 9 THRLAGLSRSGGVKSNF-VPTNVGSOAF 37

RESULT 5  
 TCRTR  
 calcitonin gene-related peptide precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 19-Feb-1984 #sequence\_revision 19-Feb-1984 #text\_change 24-Sep-1999  
 C:Accession: A01524; B22949  
 R: Amara, S.G.; Jonas, V.; Rosenfeld, M.G.; Ong, E.S.; Evans, R.M.  
 Nature 298, 240-244, 1982  
 A:Title: Alternative RNA processing in calcitonin gene expression generates mRNAs encoding  
 A:Reference number: A01524; MUID:82220111  
 A:Accession: A01524  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <AMA>  
 A:Cross-references: GB:I29188; GB:J00714; GB:N00016; NID:g457368; PIDN:AAB59682.1; PID:g  
 R:Jonas, V.; Lin, C.R.; Kawashima, E.; Semon, D.; Swanson, L.W.; Mermod, J.J.; Evans, R.  
 Proc. Natl. Acad. Sci. U.S.A. 82, 1994-1998, 1985  
 A:Title: Alternative RNA processing events in human calcitonin/calcitonin gene-related F  
 A:Reference number: A94030; MUID:85166259  
 A:Accession: B22949  
 A:Molecule type: mRNA  
 A:Residues: 1-39, 'A', 40-49, 'L', 50-67, 70-128 <JON>  
 C:Superfamily: calcitonin  
 C:Keywords: alternative splicing; amidated carboxyl end; neuropeptide  
 F:1-25/Domain: signal sequence #status predicted <SIG>  
 F:83-119/Product: calcitonin gene-related peptide #status predicted <MAT>  
 F:84-89/Disulfide bonds: #status predicted  
 F:119/Modified site: amidated carboxyl end (Phe) (amide in mature form from following gl

Query Match 82.3%; Score 123.5; DB 1; Length 128;  
 Best Local Similarity 86.7%; Pred. No. 6,9e-11;  
 Matches 26; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWSNFWPTNVGSKAF 30  
 |||||  
 Db 91 THRLAGLSRSGGVKDNF-VPTNVGSEAF 119

RESULT 6  
 A44173  
 calcitonin gene-related peptide beta precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jan-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Jul-1999  
 C:Accession: A44173; S18300  
 R:Amara, S.G.; Arizawa, J.L.; Leff, S.E.; Swanson, L.W.; Evans, R.M.; Rosenfeld, M.G.  
 Science 229, 1094-1097, 1985  
 A:Title: Expression in brain of a messenger RNA encoding a novel neuropeptide homologous

A:Reference number: A44173; MUID:85300490  
 A:Accession: A44173  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-134 <AMA>  
 A:Cross-references: GB:M11596; NID:g203232; PIDN:AAA40850.1; PID:g203233  
 A:Note: the authors translated the codon AAA for residue 47 as Phe, and CGC for resid  
 R:Wang, M.W.; Young, A.A.; Rink, T.J.; Cooper, G.J.S.  
 FEBS Lett. 291, 195-198, 1991  
 A:Title: (8-37)-CCRP antagonizes actions of amylin on carbohydrate metabolism in vit  
 A:Reference number: S18300; MUID:92038032  
 A:Accession: S18300  
 A:Molecule type: protein  
 A:Residues: 96-104, 'S', 106-112, 'N', 114-125 <MAN>  
 C:Superfamily: calcitonin  
 C:Keywords: neuropeptide

Query Match 81.7%; Score 122.5; DB 2; Length 134;  
 Best Local Similarity 86.7%; Pred. No. 1e-10;  
 Matches 26; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWSNFWPTNVGSKAF 30  
 |||||  
 Db 97 THRLAGLSRSGGVKDNF-VPTNVGSKAF 125

RESULT 7  
 B44173  
 calcitonin gene-related peptide alpha precursor - rat  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 30-Jan-1993 #sequence\_revision 12-Mar-1993 #text\_change 16-Jul-1999  
 C:Accession: B44173  
 R:Amara, S.G.; Arizawa, J.L.; Leff, S.E.; Swanson, L.W.; Evans, R.M.; Rosenfeld, M.G.  
 Science 229, 1094-1097, 1985  
 A:Title: Expression in brain of a messenger RNA encoding a novel neuropeptide homolog  
 A:Reference number: A44173; MUID:85300490  
 A:Accession: B44173  
 A>Status: preliminary  
 A:Molecule type: mRNA  
 A:Residues: 1-128 <AMA>  
 A:Cross-references: GB:M11597; NID:g203226; PIDN:AAA0847.1; PID:g203227  
 A:Note: the authors translated the codon CGC for residue 99 as Ser  
 C:Superfamily: calcitonin  
 C:Keywords: neuropeptide

Query Match 79.0%; Score 118.5; DB 2; Length 128;  
 Best Local Similarity 83.3%; Pred. No. 3,8e-10;  
 Matches 25; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWSNFWPTNVGSKAF 30  
 |||||  
 Db 91 THRLAGLSRSGGVKDNF-VPTNVGSEAF 119

RESULT 8  
 TCRTRP  
 calcitonin gene-related peptide precursor - chicken  
 C:Species: Gallus gallus (chicken)  
 C>Date: 30-Jun-1991 #sequence\_revision 30-Jun-1991 #text\_change 18-Jun-1999  
 C:Accession: S00154; I50183; A24855  
 R:Minvielle, S.; Cressent, M.; Delehay, M.C.; Segond, N.; Milhaud, G.; Jullienne, A.  
 FEBS Lett. 223, 63-68, 1987  
 A:Title: Sequence and expression of the chicken calcitonin gene.  
 A:Reference number: S00153; MUID:88030046  
 A:Accession: S00154  
 A:Molecule type: DNA  
 A:Residues: 1-125 <MIN>  
 A:Cross-references: EMBL:X06311  
 A:Note: the sequences of codons 31-33 and 34-38 are interchanged in this reference; t  
 R:Lasmoles, F.; Jullienne, A.; Day, F.; Minvielle, S.; Milhaud, G.; Moukhtar, M.S.

Query Match:	73.7%	Score 110.5;	DB 1;	Length 125;
Best Local Similarity	80.0%;	Pred. No. 5.6e-09;		
Matches 24;	Conservative 2;	Mismatches 3;	Indels 1;	Gaps 1.
<p>             QY 1 THRAGLLSRSGMVKSNFVPTNVGSKAF 30                          :                             88 THRAGFLSRSGGVKKNF-VPTNVGSKAF 116           </p>				

```
Query Match      34.7% Score 52; DB 2; Length 449;
Best Local Similarity 39.1%; Pred. NO. 9.7;
Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
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Query Match	34.08;	Score 51;	DB 1;	Length 474;
Best Local Similarity	44.48;	Pred. NO. 14;		
Matches 12; Conservative	4;	Mismatches 7;	Indels 4;	Gaps 1;

RESULT 11  
A13349

A:Accession: A13349  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-474 <KUR>  
A:Cross-references: GB:AE008917; P1DN:AAL51964.1; PID:917982723; GSPDB:GN001900  
A:Experimental source: strain 16M

Query Match	34.0%;	Score 51;	DB 2;	Length 474;
Best Local Similarity	44.4%;	Pred. No. 14;		
Matches 12;	Conservative 4;	Mismatches 7;	Indels 4;	Gaps 1;

RESULT 12  
A33542

A:Accession: A33542  
A:Molecule type: mRNA  
A:Residues: 1-89 <NS>  
A:Cross-references: NB:25388; NID:9163861; PIDN:AAA30813.1; PID:9163862  
R:Betsholtz, C.; Christmansson, L.; Engstrom, U.; Forsman, F.; Jordan, K.; O'Brien, T  
Diabetes 39, 118-122, 1990  
A:Title: Structure of cat islet amyloid polypeptide and identification of amino acid  
A:Reference number: A60499; MUID:91006862

A/Accession: A60499  
A/Status: not compared with conceptual translation  
A/Molecule type: mRNA  
A/Residues: 34-70 <BET>  
R/Westernmark, P.; Wernstedt, C.; Wilander, E.; Hayden, D.W.; O'Brien, T.D.; Johnson, P.R. Natl. Acad. Sci. U.S.A. 84, 3881-3885, 1987  
Title: Amyloid fibrils in human insulinoma and islets of Langerhans of the diabetic

A:Reference number: A26619; MUID:87231921  
 A:Accession: B26619  
 A:Status: preliminary  
 A:Molecule type: protein  
 A:Residues: 34, 'X', 36-39, 'X', 41-60 <MES>  
 C:Superfamily: calcitonin  
 C:Keywords: amidated carboxyl end; amyloid; pancreas  
 F:70/Modified site: amidated carboxyl end (Tyr) (amide in mature form from following gly

Query Match 33.7%; Score 50.5; DB 2; Length 89;  
 Best Local Similarity 43.3%; Pred. No. 2.7;

Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNVGSKAF 30  
 ||||| : : : ||||| :  
 DB 42 TORLANFLIRSSNMLGA-ILSPTNVGSNTY 70

RESULT 13  
 A56855  
 Islet amyloid polypeptide precursor - chicken

N:Alternate names: INPP

C:Species: Gallus gallus (chicken)

C:Date: 11-Aug-1995 #sequence\_revision 11-Aug-1995 #text\_change 16-Jul-1999

C:Accession: A56855

R:Fan, L.; Westermarck, G.; Chan, S.J.; Steiner, D.F.

Mol. Endocrinol. 8, 713-721, 1994

A:Title: Altered gene structure and tissue expression of islet amyloid polypeptide in th

A:Reference number: A56855; MUID:95021303

A:Accession: A56855

A:Status: preliminary

A:Molecule type: mRNA; DNA

A:Residues: 1-135 <FAN>

A:Cross-references: GB:IL6955; NID:g289789; PIDN:AAA67704.1; PID:g289790

C:Superfamily: calcitonin

C:Keywords: hormone

Query Match 33.7%; Score 50.5; DB 2; Length 135;  
 Best Local Similarity 43.3%; Pred. No. 4.3;  
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNVGSKAF 30  
 ||||| : : : ||||| :  
 DB 88 TORLADFLVRSSNMGATY-SPTNVGSNTY 116

RESULT 14  
 T04301  
 beta-expansin - rice

C:Species: Oryza sativa (rice)

C:Date: 23-Apr-1999 #sequence\_revision 23-Apr-1999 #text\_change 26-May-2000

C:Accession: T04301

R:Cosgrove, D.J.; Bedinger, P.; Duracko, D.M.

Proc. Natl. Acad. Sci. U.S.A. 94, 6559-6564, 1997

A:Title: Group I allergens of grass pollen as cell wall-loosening agents.

A:Reference number: Z15266; MUID:97322412

A:Accession: T04301

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-261 <COS>

A:Cross-references: EMBL:U95968; NID:g2224914; PIDN:AAB61710.1; PID:g2224915

C:Superfamily: expansin

Query Match 33.0%; Score 49.5; DB 2; Length 261;  
 Best Local Similarity 39.5%; Pred. No. 12;  
 Matches 15; Conservative 5; Mismatches 7; Indels 11; Gaps 2;

OY 2 HRLAG-----LISRSGGVKSNFVPTNVGSK 28  
 ||| | : : : ||| :  
 DB 220 HRLGPFSLRWYSESGQTVIAHOVIIPANWRANTVNGSK 257

RESULT 15

A24434

beta fimbrial protein precursor - Moraxella bovis

N:Alternate names: beta pillin

C:Species: Moraxella bovis

C:Date: 08-Aug-1987 #sequence\_revision 08-Aug-1987 #text\_change 26-Aug-1999

C:Accession: A24434; J10072

R:Marrs, C.F.; Schoolnik, G.; Koomey, J.M.; Hardy, J.; Rothbard, J.; Falkow, S.

J. Bacteriol. 163, 132-139, 1985

A:Reference number: A24434; MUID:85234350

A:Accession: A24434

A:Molecule type: DNA

A:Residues: 1-157 <MAR>

A:Cross-references: GB:M11435; NID:g149760; PIDN:AAA25304.1; PID:g149761

A:Experimental source: strain EPP63

R:Ruethl, W.W.; Marrs, C.F.; Fernandez, R.; Falkow, S.; Schoolnik, G.K.

J. Exp. Med. 168, 983-1002, 1988

A:Title: Purification, characterization, and pathogenicity of Moraxella bovis pill.

A:Reference number: J10071; MUID:89010522

A:Accession: J10072

A:Molecule type: protein

A:Residues: 7-86, 93-122 <RUE>

A:Note: about 50% of the amino-terminus is N-methylated; the remaining 50% of the mol

C:Superfamily: gonococcal fimbrial protein

C:Keywords: methylated amino end; surface antigen

F:1-6/Domain: propioid #status predicted <PRO>

F:1-157/Product: beta fimbrial protein 1 #status experimental <MAT>

F:8-157/Product: beta fimbrial protein 2 #status experimental <MA2>

F:7/Modified site: methylated amino end (Phe) (in mature form) #status experimental

F:136-155/Disulfide bonds: #status experimental

Query Match 32.7%; Score 49; DB 2; Length 157;  
 Best Local Similarity 39.1%; Pred. No. 8.4;  
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

OY 8 LSRSGGVKSNFVPTNVGSKAF 30  
 ||: ||| : || : ||| :  
 DB 78 LTTTGGTARSNLMSSVNIIGGAF 100

Search completed: August 26, 2002, 15:52:37  
 Job time: 129 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 26, 2002, 15:50:48 ; Search time 25.2 Seconds  
(without alignments)  
205.946 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150  
Sequence: 1 THRLAGLSRSGWVKNFVPTNVGSKAF 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protist:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriophage:\*  
17: sp\_archaeal:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	124.5	83.0	128	6	Q9MYV1
2	123.5	82.3	128	11	Q99JAO
3	122.5	81.7	129	6	Q9NCT3
4	116.5	77.7	67	6	Q9GAK2
5	109.5	73.0	52	13	P79814
6	108.5	72.3	130	11	Q99MP3
7	106.5	71.0	56	13	Q92164
8	105.5	70.3	60	6	Q9GLK1
9	101.5	67.7	53	13	Q90YC3
10	78.5	52.3	127	6	Q9NOT2
11	36	37.3	223	5	Q9V9B4
12	52	34.7	144	11	Q9WVF6
13	52	34.7	407	2	Q9FC90
14	52	34.7	449	5	Q01762
15	52	34.7	605	5	Q9VM60
16	51	34.0	474	2	Q44596

17	50.5	33.7	135	13	Q90743	Q90743 gallus gall
18	50.5	33.7	4003	2	Q9RFLO	Q9RFLO stigmatella
19	49.5	33.0	261	10	Q9AV20	Q9AV20 oryza sativ
20	49.5	33.0	261	10	Q24230	Q24230 oryza sativ
21	49	32.7	190	5	Q25180	Q25180 heliopsis v
22	49	32.7	388	2	Q9E066	Q9E066 escherichia
23	49	32.7	388	2	Q9F6H3	Q9F6H3 escherichia
24	49	32.7	388	2	Q9F6H1	Q9F6H1 escherichia
25	49	32.7	1029	2	Q52708	Q52708 rickettsia
26	48.5	32.3	834	2	Q52647	Q52647 rickettsia
27	48	32.0	343	2	Q9F6H4	Q9F6H4 escherichia
28	48	32.0	388	2	Q9F6G8	Q9F6G8 escherichia
29	48	32.0	388	2	Q9F6G6	Q9F6G6 escherichia
30	48	32.0	388	2	Q9F6G4	Q9F6G4 escherichia
31	48	32.0	388	2	Q9F6G3	Q9F6G3 escherichia
32	48	32.0	388	2	Q9F6G2	Q9F6G2 escherichia
33	48	32.0	388	2	Q9F6G1	Q9F6G1 escherichia
34	48	32.0	388	2	Q9F6F9	Q9F6F9 escherichia
35	48	32.0	388	2	Q9F6F7	Q9F6F7 escherichia
36	48	32.0	388	2	Q9F6F5	Q9F6F5 escherichia
37	48	32.0	388	2	Q9F6F4	Q9F6F4 escherichia
38	48	32.0	388	2	Q9F6F3	Q9F6F3 escherichia
39	48	32.0	388	2	Q9F6F2	Q9F6F2 escherichia
40	48	32.0	875	2	Q86174	Q86174 bacteroides
41	47.5	31.7	336	10	Q944F5	Q944F5 oryza sativ
42	47.5	31.7	385	16	Q97EP2	Q97EP2 clostridium
43	47	31.3	428	16	Q98N31	Q98N31 rhizobium l
44	47	31.3	694	10	Q9LSC3	Q9LSC3 arabidopsis
45	47	31.3	995	16	Q9HY75	Q9HY75 pseudomonas

## ALIGNMENTS

RESULT	ID	PRELIMINARY	PRT	128 AA.
Q9MYV1	Q9MYV1	Q9MYV1		
AC	Q9MYV1	Q9MYV1		
DT	01-OCT-2000 (TREMBLrel. 15, Created)			
DT	01-OCT-2000 (TREMBLrel. 15, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	PREPRO-ALPHA-CALCITONIN GENE-RELATED PEPTIDE PRECURSOR.			
GN	CCALCT.			
OS	Canis familiaris (Dog).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.			
OX	NCBI_TaxID=9615;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-20353881; PubMed-10895326;			
RA	Wende S., Kremppler A., Brenig B.;			
RT	*Detection of a polymorphic 27 bp insertion/deletion in exon 4 of the			
RT	canine calcitonin/calcitonin gene-related peptide gene 1.;			
RL	Anim. Genet. 31:238-239(2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE-20424786; PubMed-10967131;			
RA	Wende S., Kremppler A., Breen M., Brunberg L., Brenig B.;			
RT	*Molecular analysis and chromosomal assignment of the canine CALC-			
RT	I/alpha-CGRP gene.;			
RL	Mamm. Genome 11:736-740(2000).			
DR	EMBL; AJ271090; CAB97487.1; .			
DR	InterPro: IPR002163; Calcitonin beta.			
DR	InterPro: IPR001693; Calc CGRP IAP.			
DR	InterPro: IPR000443; Islet amyloid.			
DR	Pfam; PF00214; Calc_CGRP_IAP; 1.			
DR	PRINTS; PR00817; CALCITONINB.			
DR	PRINTS; PR00818; ISLETAMYLOID.			
DR	SMART; SM00113; CALCITONIN; 1.			
KW	PROSITE; PS00258; CALCITONIN; 1.			
FT	SIGNAL.			
FT	SIGNAL	1	84	POTENTIAL.
FT	SIGNAL	1	82	POTENTIAL.

FT CHAIN 83 128 ALPHA-CALCITONIN GENE-RELATED PEPTIDE.  
SQ SEQUENCE 128 AA; 13874 MW; 72331258DB8CB564 CRC64;

Query Match 83.0%; Score 124.5; DB 6; Length 128;  
Best Local Similarity 86.7%; Pred. No. 2,8e-11;  
Matches 26; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGKVSFVPTNGSKAF 30  
|||||  
DB 91 THRLAGLSRSGGVKNF-VPTNGSEAF 119

## RESULT 2

ID 099JA0 PRELIMINARY; PRT; 128 AA.  
AC 099JA0;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE ALPHA-TYPE CALCITONIN GENE-RELATED PEPTIDE PRECURSOR.  
GN CALCA OR CALC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Sarasa M., Catalan J., Aramayo J., Sorribas V.;  
RT "Mouse CGRP precursor is highly homologous to that of the rat."  
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129/SVEV;  
RA Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;  
RT "Structure of the Mouse Calcitonin/Calcitonin Gene-Related Peptide  
RT Alpha and Beta Genes.";  
RL DNA Seq. 0:0-0(2001).  
DR EMBL; AF330212; AAK06841.1; -;  
DR EMBL; AF335522; AAK18181.1; -;  
DR EMBL; AF335521; AAK18181.1; JOINED.  
DR MGI; MGI:2151253; Calca.  
DR InterPro: IPR002163; Calcitonin\_beta.  
DR InterPro: IPR001693; Calc\_CGRP\_IAPP.  
DR InterPro: IPR000443; Islet\_amyloid.  
DR Pfam: PF00214; Calc\_CGRP\_IAPP; 1.  
DR PRINTS; PR00817; CALCITONINB.  
DR PRINTS; PR00818; ISLETAMYLTD.  
DR SMART; SM00113; CALCITONIN; 1.  
DR PROSITE; PS00258; CALCITONIN; 1.  
FT CHAIN 83 119 ALPHA-TYPE CALCITONIN GENE-RELATED  
FT PEPTIDE PRECURSOR.  
SQ SEQUENCE 128 AA; 14065 MW; 83BB0E36C8B4239E CRC64;

Query Match 82.3%; Score 123.5; DB 11; Length 128;  
Best Local Similarity 86.7%; Pred. No. 4e-11;  
Matches 26; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGKVSFVPTNGSKAF 30  
|||||  
DB 91 THRLAGLSRSGGVKNF-VPTNGSEAF 119

## RESULT 3

ID 09NOT3 PRELIMINARY; PRT; 129 AA.  
AC 09NOT3;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CALCITONIN GENE RELATED PEPTIDE II PRECURSOR.  
OS Equus caballus (Horse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
OX NCBI\_TaxID=9796;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Toribio R.E., Kohn C.W., Chew D.J., Rosol T.J.;  
RT "Molecular Cloning of Equine Calcitonin and Calcitonin Gene Related  
RT Peptide."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF257470; AAF70199.1; -;  
DR InterPro: IPR002163; Calcitonin\_beta.  
DR InterPro: IPR001693; Calc\_CGRP\_IAPP.  
DR InterPro: IPR000443; Islet\_amyloid.  
DR Pfam: PF00214; Calc\_CGRP\_IAPP; 1.  
DR PRINTS; PR00817; CALCITONINB.  
DR PRINTS; PR00818; ISLETAMYLTD.  
DR SMART; SM00113; CALCITONIN; 1.  
DR PROSITE; PS00258; CALCITONIN; 1.  
KM Signal.  
FT SIGNAL 1 25 POTENTIAL.  
FT CHAIN 84 120 CALCITONIN GENE RELATED PEPTIDE II.  
SQ SEQUENCE 129 AA; 13925 MW; 97C27AC713ABD9B CRC64;

Query Match 81.7%; Score 122.5; DB 6; Length 129;  
Best Local Similarity 86.7%; Pred. No. 5,8e-11;  
Matches 26; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGKVSFVPTNGSKAF 30  
|||||  
DB 92 THRLAGLSRSGGVKNF-VPTDVGSEAF 120

## RESULT 4

ID 09GLK2 PRELIMINARY; PRT; 67 AA.  
AC 09GLK2;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)  
DE CALCITONIN GENE-RELATED PEPTIDE VARIANT 1 (FRAGMENT).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_TaxID=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Davis M.C., Gierasch W.W., Russo A.F.;  
RT "Rabbit calcitonin gene-related peptide partial cDNA for exons 3 and  
RT 5, variant allele 1."  
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF260272; AAG15535.1; -;  
DR InterPro: IPR002163; Calcitonin\_beta.  
DR InterPro: IPR001693; Calc\_CGRP\_IAPP.  
DR InterPro: IPR000443; Islet\_amyloid.  
DR Pfam: PF00214; Calc\_CGRP\_IAPP; 1.  
DR PRINTS; PR00817; CALCITONINB.  
DR PRINTS; PR00818; ISLETAMYLTD.  
DR SMART; SM00113; CALCITONIN; 1.  
DR PROSITE; PS00258; CALCITONIN; 1.  
FT NON\_TER 1 67  
FT NON\_TER 1 67  
SQ SEQUENCE 67 AA; 7286 MW; 99CG326C159BC501 CRC64;

Query Match 77.7%; Score 116.5; DB 6; Length 67;  
Best Local Similarity 96.2%; Pred. No. 2,3e-10;  
Matches 25; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGKVSFVPTNG 26  
|||||  
DB 42 THRLAGLSRSGGKVSFVPTNG 66



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RESULT 5
P79814 PRELIMINARY; PRT; 52 AA.
ID P79814
AC P79814
DT 01-MAY-1997 (TREMBLrel. 03, Created)
DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE 4 (FRAGMENT).
DE Oncorhynchus gorbuscha (Pink salmon) (Humpback salmon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8017;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97057244; PubMed=8901583;
RA Jansz H., Martial K., Zandberg J., Milnaud G., Benson A.A.,
RA Juliette A., Moukhtar M.S., Cressent M.;
RT "Identification of a new calcitonin gene in the salmon Oncorhynchus
RT gorbuscha.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:12344-12348(1996).
DR EMBL: U71287; AAB38533.1; -.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR Pfam: PF00214; Calc_CGRP_IAPP.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1 1
FT CHAIN 1 4 N-TERMINAL PEPTIDE.
FT CHAIN 7 43 CALCITONIN GENE-RELATED PEPTIDE 4.
FT CHAIN 49 52 CARBOXY TERMINAL PEPTIDE.
SQ SEQUENCE 52 AA; 5700 MW; 3F4C471D2A682321 CRC64;

Query Match 73.0%; Score 109.5; DB 13; Length 52;
Best Local Similarity 80.0%; Pred. No. 2e-09;
Matches 24; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 THRAGLILSRSGMVKSNFVPTNGSKAF 30
Db 15 THRAGLILSRSGMVKSNFVPTNGAKAF 43

RESULT 6
Q99MP3 PRELIMINARY; PRT; 130 AA.
ID Q99MP3
AC Q99MP3
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN/CALCITONIN-RELATED PEPTIDE BETA.
GN CALCB.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=129/SEV;
RA Thomas P.M., Nasonkin I., Zhang H., Gagel R.F., Cote G.J.;
RT "Structure of the Mouse Calcitonin/Calcitonin Gene-Related Peptide
RT Alpha and Beta Genes.";
RL DNA Seq. 0:0-0(2001).
DR EMBL: AF325526; AAK16431.1; -.
DR MBL: AF325524; AAK16431.1; JOINED.
DR MGD: MGI:2151254; Calcd.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.

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DR PRINTS: PR00818; ISLETAMYL0ID.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
SQ SEQUENCE 130 AA; 14623 MW; 97299244E9FC536 CRC64;

Query Match 72.3%; Score 108.5; DB 11; Length 130;
Best Local Similarity 76.7%; Pred. No. 8e-09;
Matches 23; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 1 THRAGLILSRSGMVKSNFVPTNGSKAF 30
Db 92 THRAGLILSRSGMVKSNFVPTNGSEAF 120

RESULT 7
Q92164 PRELIMINARY; PRT; 56 AA.
ID Q92164
AC Q92164
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
GN CGRP.
OS Oncorhynchus sp. (Salmon).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8025;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92344325; PubMed=1637123;
RA Jansz H.S., Zandberg J.;
RT "Identification and partial characterization of the salmon
RT calcitonin/CGRP gene by polymerase chain reaction.";
RL Ann. N.Y. Acad. Sci. 657:63-69(1992).
DR EMBL: S40497; AAB22593.1; -.
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1 1
SQ SEQUENCE 56 AA; 6019 MW; C7852837BAFE74314 CRC64;

Query Match 71.0%; Score 106.5; DB 13; Length 56;
Best Local Similarity 76.7%; Pred. No. 6.4e-09;
Matches 23; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 THRAGLILSRSGMVKSNFVPTNGSKAF 30
Db 15 THRAGLILSRSGMVKSNFVPTNGAKAF 43

RESULT 8
Q9GLK1 PRELIMINARY; PRT; 60 AA.
ID Q9GLK1
AC Q9GLK1
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Davis M.C., Giersch W.W., Russo A.F.;
RT "Rabbit calcitonin gene-related peptide partial cDNA for exons 3 and
RT 5.";

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RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF260273; AAG15536.1;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_Amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
DR PROSITE: PS00258; CALCITONIN; 1.
FT NON_TER 1 1
FT CHAIN 60 60
SQ SEQUENCE 60 AA: 6485 MW: 5D8A512A4E8994AE CRC64;

Query Match
Best Local Similarity 70.3%; Score 105.5; DB 6; Length 60;
Matches 23; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVG 26
DB 35 THRLADLLSRSGVYKSNF-VPTNVG 59

RESULT 9
Q09YC3 PRELIMINARY; PRT; 53 AA.
AC Q09YC3:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE (FRAGMENT).
OS Paratichthys olivaceus (Flounder).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Acanthomorpha; Acanthopterygii; Perciformes; Pleuronectiformes;
OC Pleuronectidae; Paratichthyidae; Paratichthys.
OX NCBI_TaxID=8255;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21406117; PubMed=11514025;
RA Suzuki N., Suzuki T., Kurokawa T.;
RT "Cloning of a calcitonin gene-related peptide from genomic DNA and its
RT mRNA expression in flounder, Paratichthys olivaceus.";
RL Peptides 22:1435-1438(2001).
DR EMBL: AB052782; BAB64411.1;
FT NON_TER 1 1
FT CHAIN 6 44
SQ SEQUENCE 53 AA: 5684 MW: 14C0191868A64CF4 CRC64;

Query Match
Best Local Similarity 67.7%; Score 101.5; DB 13; Length 53;
Matches 22; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVGSKAF 30
DB 16 THRLADLLSRSGVYKSNF-VPTNVGAQAF 44

RESULT 10
Q09OT2 PRELIMINARY; PRT; 127 AA.
AC Q09OT2:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
DE CALCITONIN GENE-RELATED PEPTIDE I PRECURSOR.
OS Equus caballus (Horse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
OX NCBI_TaxID=9796;

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RN [1]
RP SEQUENCE FROM N.A.
RA Toribio R.E., Kohn C.W., Chew D.J., Rosol T.J.;
RT "Molecular Cloning of Equine Calcitonin and Calcitonin-Gene Related
RT Peptides".
RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF251471; AAF70200.1;
DR InterPro: IPR002163; Calcitonin_beta.
DR InterPro: IPR001693; Calc_CGRP_IAPP.
DR InterPro: IPR000443; Islet_Amyloid.
DR Pfam: PF00214; Calc_CGRP_IAPP; 1.
DR PRINTS: PR00817; CALCITONINB.
DR SMART: SM00113; CALCITONIN; 1.
FT SIGNAL 1 25
FT CHAIN 82 118
SQ SEQUENCE 127 AA: 13864 MW: BA570B2AB49A6730 CRC64;

Query Match
Best Local Similarity 52.3%; Score 78.5; DB 6; Length 127;
Matches 17; Conservative 4; Mismatches 6; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMKVSNFVPTNVGSK 28
DB 90 THRLAGLSRSGMANSN-LTPTEMGFK 116

RESULT 11
Q09VB4 PRELIMINARY; PRT; 223 AA.
AC Q09VB4:
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE CG3403 PROTEIN.
GN CG3403.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Abghavani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballieu R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA Burlis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup I.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Kapen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Mlshina N.V., Moadary C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleib J.M.,

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RL Genes Immun. 1:191-199(2000).  
RN [5]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=THYMUS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondou S., Yamataka I.,  
RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., Kling B., Kochiwa H.,  
RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Anon H., Baldarelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carinci P., de Bonaldo M.F.,  
RA Brownstein M.T., Bult C., Flecher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli V., Mombearts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitlaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsuki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection."  
RL Nature 409:685-690(2001).  
DR EMBL: AF124374; AAD42773.1; -  
DR EMBL: AF188624; AAF09019.1; -  
DR EMBL: AF112983; AAD51391.1; -  
DR EMBL: AF169407; AAF42987.1; -  
DR EMBL: AK018005; BAB31033.1; -  
DR HSSP: P24605; 1CLP.  
DR MGD: MG1:1341796; Pla2g2d.  
DR InterPro: IPRO01211; PLP\_A2.  
DR Pfam: PF00068; phoslip; 1.  
DR PRINTS: PR00389; PHPLIPASEA2.  
DR ProDom: PD000303; PLP\_A2; 1.  
DR SMART: SM00085; PA2c; 1.  
DR PROSITE: PS00119; PA2\_ASP; 1.  
DR PROSITE: PS00118; PA2\_HIS; 1.  
KW Hydrolase.  
SQ SEQUENCE 144 AA; 16164 MW; 7697DA07F8D270A CRC64;

Query Match 34.7%; Score 52; DB 11; Length 144;  
Best Local Similarity 40.7%; Pred. NO. 3.9;  
Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0.

Oy 4 LAGLSRSGMYKSNFEVPTNYGSKAF 30  
|||:: ||:: |:: |:: ||||  
Db 11 LAGTATGGGLNLNKNKYHTGTAKAF 37

RESULT 13  
Q9FC90  
ID O9FC90 PRELIMINARY; PRT; 407 AA.  
AC O9FC90;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ORNITHINE AMINOTRANSFERASE.  
GN ROD.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycetaceae; Streptomycetaceae; Streptomycetes.  
CX NCBI\_TaxId=1902;  
[1]  
RN SEQUENCE FROM N.A.  
RP STRAIN=A3(2);  
RC Saunders D.C., Harris D.;  
RL Submitted (Aug-2000) to the EMBL/GenBank/DDBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A3(2);

RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-A3(2);  
 RX MEDLINE-97000351; PubMed-8843436;  
 RA Kedenbach M., Kleier H.M., Denaplatte D., Elchner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb Streptomyces coelicolor A3(2) chromosome";  
 RL Mol. Microbiol. 21:77-96(1996).  
 DR EMBL: AL391017; CAC01505.1; -.  
 DR HSSP: P04181; 20RT.  
 DR InterPro: IPR000954; AminoTran\_3.  
 DR Pfam: PF00202; aminoTran\_3.  
 DR PROSITE: PS00600; AA\_TRANSFER\_CLASS\_3; 1.  
 KW Transferase; AminoTransferase.  
 SQ SEQUENCE 407 AA; 42906 MW; C808C409C73B56DF CRC64;

Query Match 34.7%; Score 52; DB 2; Length 407;  
 Best Local Similarity 37.0%; Pred. No. 12;  
 Matches 10; Conservative 6; Mismatches 11; Indels 0; Gaps 0;

OY 3 RLASRGWKSNEFVPTNGSKA 29  
 DB 90 RLAGEAERLALTDVLPMTNGAFA 116

RESULT 14  
 ID 001762 PRELIMINARY; PRT; 449 AA.  
 AC 001762;  
 DT 01-NOV-1996 (TREMBLrel. 01, Created)  
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE CELLULOSE.  
 GN PCCH1-1.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OX NCBI\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BKM-1767;  
 RX MEDLINE-93046812; PubMed-1423728;  
 RT Covert S.F., Bolduc J., Cullen D.;  
 RT "Genomic organization of a cellulase gene family in Phanerochaete  
 RT chrysosporium";  
 RL Curr. Genet. 22:407-413(1992).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BKM-1767;  
 RX MEDLINE-92344372; PubMed-1637155;  
 RA Covert S.F., Vanden Wymelenberg A., Cullen D.;  
 RT "Structure, organization, and transcription of a cellobiohydrolase  
 RT gene cluster from Phanerochaete chrysosporium";  
 RL Appl. Environ. Microbiol. 58:2168-2175(1992).  
 DR EMBL: X54411; CAA38274.1; -.  
 DR HSSP: P00725; 8CEL.  
 DR InterPro: IPR001722; Glyco\_hydro\_7.  
 DR Pfam: PF00840; Glyco\_hydro\_7; 1.  
 DR ProDom: PD186135; Glyco\_hydro\_7; 1.  
 SQ SEQUENCE 449 AA; 47348 MW; DE6455127BFF133C CRC64;

Query Match 34.7%; Score 52; DB 3; Length 449;  
 Best Local Similarity 39.1%; Pred. No. 14;  
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;

OY 8 LRSRGWKSNEFVPTNGSKAF 30  
 DB 103 ITTSGALRLQFVLTGNTIGSRVF 125

RESULT 15  
 ID 09YM60 PRELIMINARY; PRT; 605 AA.  
 AC 09YM60;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE CG3430 PROTEIN.  
 GN CG3430.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;  
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BERKELEY;  
 RX MEDLINE-20196006; PubMed-10731132;  
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,  
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,  
 RA Sutton R.C., Wortman J.R., Fandell M.D., Zhang Q., Chen L.X.,  
 RA Brandon R.C., Rogers Y.-H.C., Blazer J.R., Champe M., Pfeiffer B.D.,  
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,  
 RA April J.F., Abmayyan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,  
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,  
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,  
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,  
 RA Burtis K.C., Busam D.A., Butler H., Cadien E., Center A., Chandra I.,  
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,  
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,  
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,  
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,  
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,  
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,  
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,  
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,  
 RA Jallali M., Kalush F., Karpen G.H., Ke Z., Kensington J.A., Ketchum K.A.,  
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,  
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,  
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,  
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,  
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,  
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Paclebo J.M.,  
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,  
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,  
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,  
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,  
 RA Sylvestras R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,  
 RA Wang Z.-Y., Wasserman D., Weinstock K.C., Wu D., Yang S., Yao Q.A.,  
 RA Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 DR EMBL: AE003615; AAP52465.1; -.  
 DR FlyBase: FBgn0031875; CG3430.  
 SQ SEQUENCE 605 AA; 68016 MW; E89C45FD96B2B630 CRC64;

Query Match 34.7%; Score 52; DB 5; Length 605;  
 Best Local Similarity 47.8%; Pred. No. 19;  
 Matches 11; Conservative 4; Mismatches 8; Indels 0; Gaps 0;

OY 7 LRSRGWKSNEFVPTNGSKA 29  
 DB 469 VLSEGRSMLEPSDFVLPINADSKA 491

Search completed: August 26, 2002, 15:53:09  
Job time: 141 sec

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# OM protein - protein search, using sw model

Run on: August 26, 2002, 15:51:24 ; Search time 10.42 Seconds  
(without alignments)  
111.477 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150  
Sequence: 1 THRAGLSRSGMKNFVPTNGSKAF 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SWISSProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	135.5	90.3	127	1 CAL2_HUMAN	P10092 homo sapien
2	128.5	85.7	128	1 CAL1_HUMAN	P06881 homo sapien
3	127.5	85.0	37	1 CGRP_SHEEP	P30881 ovis aries
4	126.5	84.3	37	1 CGRP_PIG	P30880 sus scrofa
5	123.5	82.3	128	1 CAL1_RAT	P01256 rattus norv
6	122.5	81.7	134	1 CAL2_RAT	P10093 rattus norv
7	117.5	78.3	37	1 CGRP_RANRI	P13888 rana ridibu
8	110.5	73.7	125	1 CALR_CHICK	P10286 gallus gall
9	68.5	45.7	115	1 CGRP_PHYBI	P1564 pyllomedus
10	53.5	35.7	32	1 IAPP_SAGE	Q28934 saguinus,oe
11	52	34.7	144	1 PA2D_MOUSE	Q28934 mus musculu
12	50.5	33.7	89	1 IAPP_FELCA	P12967 felis silve
13	49	32.7	157	1 FMO_MORBO	P07640 moraxella b
14	49	32.7	516	1 GUX1_PHACH	P13860 phanerochae
15	48.5	32.3	93	1 IAPP_MOUSE	P12968 mus musculu
16	48.5	32.3	93	1 IAPP_RAT	P12969 rattus norv
17	48	32.0	428	1 THRC_ECOLI	P00934 escherichia
18	48	32.0	429	1 OGRA_MYCU	O10387 mycobacteri
19	48	32.0	533	1 PRGS_BORBU	O51522 borrelia bu
20	48	32.0	1609	1 RPRO_TMCAV	P18339 tobacco mil
21	48	32.0	2021	1 OMPA_RICCN	Q25657 rickettsia
22	47.5	31.3	89	1 IAPP_CANFA	P17716 canis famli
23	47	31.3	833	1 PTIA_ECOLI	P32670 escherichia
24	46.5	31.0	230	1 EBP_MOUSE	P70245 mus musculu
25	46	30.7	258	1 ARGB_BACSU	P36840 bacillus su
26	46	30.7	434	1 Y181_MYCN	Q05292 mycoplasma
27	46	30.7	2249	1 OMPA_RICCN	P15921 rickettsia
28	45.5	30.3	37	1 IAPP_CRIGR	P19890 cricetulus
29	45.5	30.3	92	1 IAPP_MESAU	P23442 mesocricetu
30	45	30.0	159	1 MYFA_YEREN	P33406 yersinia en
31	45	30.0	242	1 HYPB_HELPJ	O25560 helicobacte
32	45	30.0	242	1 HYPB_HELPJ	O25560 helicobacte
33	45	30.0	429	1 THRC_BUCAL	P57289 buchnera ap

34	45	30.0	489	1 CPCU_RABIT	Q29510 oryctolagus
35	45	30.0	748	1 JSBL_TRINI	Q06342 trichoplusi
36	44.5	29.7	522	1 GSHL_ARATH	P46309 arabidopsis
37	44.5	29.7	3023	1 POLG_TYMY	P09814 t genome po
38	44	29.3	429	1 THRC_SERMA	P27735 serritella ma
39	44	29.3	439	1 RCA2_TOBAC	Q40565 nicotiana t
40	44	29.3	442	1 RCAL_TOBAC	Q40460 nicotiana t
41	44	29.3	575	1 IIVB_LACLA	Q02137 lactococcus
42	44	29.3	1116	1 VP2_RDVF	O98632 rice dwarf
43	44	29.3	1222	1 PMSR_HUMAN	O15155 homo sapien
44	44	29.3	1612	1 RPRO_ORSVS	O84133 odonogloss
45	44	29.3	2491	1 MPRL_HUMAN	P11717 homo sapien

## ALIGNMENTS

RESULT	1	STANDARD	PRT	127 AA
ID	CAL2_HUMAN			
AC	P10092; O9UCN9;			
DT	01-MAR-1989 (rel. 10, Created)			
DT	01-MAR-1989 (rel. 10, Last sequence update)			
DT	16-OCT-2001 (rel. 40, Last annotation update)			
DE	Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type CGRP).			
DE	CALCB OR CALC2.			
GN	Calcitonin Receptor-Like Receptor 2 (CALCRL2)			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=87105923; PubMed=3492393;			
RA	Steenbergh P.H., Hoepener J.W.M., Zandberg J., Vlaser A.,			
RA	Lips C.J.M., Jansz H.S.;			
RT	"Structure and expression of the human calcitonin/CGRP genes.";			
RL	FEBS Lett. 209:97-103(1986).			
RN	[2]			
RP	SEQUENCE OF 56-127 FROM N.A.			
RX	MEDLINE=85180007; PubMed=2985435;			
RA	Steenbergh P.H., Hoepener J.W.M., Zandberg J., Lips C.J.M.,			
RA	Jansz H.S.;			
RT	"A second human calcitonin/CGRP gene.";			
RL	FEBS Lett. 183:403-407(1985).			
RN	[3]			
RP	PARTIAL SEQUENCE OF 82-108.			
RX	MEDLINE=87109142; PubMed=3492492;			
RA	Petermann J.B., Born W., Chang J.Y., Fischer J.A.;			
RT	"Identification in the human central nervous system, pituitary, and			
RT	thyroid of a novel calcitonin gene-related peptide, and partial amino			
RT	acid sequence in the spinal cord.";			
RL	J. Biol. Chem. 262:542-545(1987).			
RN	[4]			
RP	SEQUENCE OF 82-86 AND 104-117.			
RX	TISSUE-Spinal cord.			
RA	MEDLINE=90211348; PubMed=2322288;			
RA	Wimalawansa S.J., Morris H.R., Etienne A., Blench I., Panico M.,			
RA	McIntyre I.;			
RT	"Isolation, purification and characterization of beta-hCGRP from			
RT	human spinal cord.";			
RL	Biochem. Biophys. Res. Commun. 167:993-1000(1990).			
RN	[5]			
RP	SEQUENCE OF 82-104.			
RX	TISSUE-Pheochromocytoma;			
RA	MEDLINE=92287083; PubMed=1318039;			
RA	Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T.;			
RT	"Isolation and characterization of peptides which act on rat			
RT	platelets, from a pheochromocytoma.";			
RL	Biochem. Biophys. Res. Commun. 185:134-141(1992).			
CC	"FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF			
CC	VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.			
CC	ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR			

CC NEURONMODULATOR ROLE.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X04855; CAC05295.1; -  
 DR EMBL: X04857; CAC05295.1; JOINED.  
 DR EMBL: X04861; CAC05295.1; JOINED.  
 DR EMBL: X02404; CAC05295.1; -  
 DR PIR: A25864; A25864.  
 DR PIR: A34565; A34565.  
 DR PIR: B26142; B26142.  
 DR MIM: 114160; -  
 DR InterPro: IPR001693; Calc-CGRP\_IAPP.  
 DR InterPro: IPR002163; Calcitonin\_beta.  
 DR Pfam: PF00214; Calc-CGRP\_IAPP.1.  
 DR PRINTS: PR00817; CALCITONINB.  
 DR SMART: SM00113; CALCITONIN.1.  
 DR PROSITE: PS00256; CALCITONIN.1.  
 DR Cleavage on pair of basic residues; Amidation; Hormone; Signal.  
 KM SIGNAL 1 25 POTENTIAL.  
 FT PROPEP 26 79  
 FT PEPTIDE 82 118 CALCITONIN GENE-RELATED PEPTIDE II.  
 FT PROPEP 124 127  
 FT DISULFID 83 88  
 FT MOD\_RES 118 118 AMIDATION (G-119 PROVIDE AMIDE GROUP).  
 FT CONFLICT 73 73 G -> S (IN REF. 2).  
 SQ SEQUENCE 127 AA; 13706 MW; B0A71A063CD5ACE7 CRC64;  
 QY 1 THRLAGLLSRSGWVKSNFVPTNVGSKAF 30  
 Db 90 THRLAGLLSRSGWVKSNF-VPTNVGSKAF 118  
 Query Match 90.3%; Score 135.5; DB 1; Length 127;  
 Best Local Similarity 96.7%; Prid. No. 1.6e-13;  
 Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;  
 RESULT 2  
 ID CALI\_HUMAN STANDARD; PRT; 128 AA.  
 AC P06881; Q93048; Q9UCP0;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-MAR-1989 (Rel. 10, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type  
 DE CGRP).  
 GN CALCA OR CALCI.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxId=9606;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89386053; PubMed=2571128;  
 RA Broad P.M., Symes A.J., Thakker R.V., Craig R.K.;  
 RT "Structure and methylation of the human calcitonin/alpha-CGRP gene.";  
 RL Nucleic Acids Res. 17:6599-7011(1989).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=85166259; PubMed=3872459;  
 RA Jones V., Lin C.R., Kawashima E., Semon D., Swanson L.W.,  
 RA Mermel J.-J., Evans R.M., Rosenfeld M.G.;  
 RT "Alternative RNA processing events in human calcitonin/calcitonin  
 RT gene-related peptide gene expression.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).

RN (3)  
 RP SEQUENCE OF 48-119 FROM N.A.  
 RX MEDLINE=85022523; PubMed=6148938;  
 RA Nelkin B.D., Rosenfeld K.I., de Bustros A., Leong S.S., Roos B.A.,  
 RA Bayliss S.B.;  
 RT "Structure and expression of a gene encoding human calcitonin and  
 RT calcitonin gene related peptide.";  
 RL Biochem. Biophys. Res. Commun. 123:648-655(1984).  
 RN (4)  
 RP SEQUENCE OF 49-128 FROM N.A.  
 RX MEDLINE=85230541; PubMed=2408883;  
 RA Edbrooke M.R., Parker D., McVey J.H., Riley J.H., Sorenson G.D.,  
 RA Pettengill O.S., Craig R.K.;  
 RT "Expression of the human calcitonin/CGRP gene in lung and thyroid  
 RT carcinoma.";  
 RL EMBO J. 4:715-724(1985).  
 RN (5)  
 RP SEQUENCE OF 77-128 FROM N.A.  
 RC TISSUE=Thyroid carcinoma;  
 RX MEDLINE=84240176; PubMed=6610687;  
 RA Steenberg P.H., Hopener J.W., Zandberg J., de Ven W.J., Jansz H.S.,  
 RA Lips C.J.;  
 RT "Calcitonin gene related peptide coding sequence is conserved in the  
 RT human genome and is expressed in medullary thyroid carcinoma";  
 RL J. Clin. Endocrinol. Metab. 59:358-360(1984).  
 RN (6)  
 RP SEQUENCE OF 77-128 FROM N.A.  
 RX MEDLINE=87213363; PubMed=3034287;  
 RA Craig R.K., Riley J.H., Edbrooke M.R., Broad P.M., Poord S.M.,  
 RA Al-Kazwini S.J., Holman J.J., Marshall I.;  
 RT "Expression and function of the human calcitonin/alpha-CGRP gene in  
 RT health and disease";  
 RL Biochem. Soc. Symp. 52:91-105(1986).  
 RN (7)  
 RP SEQUENCE OF 83-119.  
 RX MEDLINE=84191466; PubMed=6609312;  
 RA Morris H.R., Panico M., Etienne T., Tipples J., Garg S.I.,  
 RA McIntyre I.;  
 RT "Isolation and characterization of human calcitonin gene-related  
 RT peptide.";  
 RL Nature 308:746-748(1984).  
 RN (8)  
 RP PARTIAL SEQUENCE OF 83-117.  
 RX MEDLINE=87109142; PubMed=3492492;  
 RA Petermann J.B., Born W., Chang J.Y., Fischer J.A.;  
 RT "Identification in the human central nervous system, pituitary, and  
 RT thyroid of a novel calcitonin gene-related peptide, and partial amino  
 RT acid sequence in the spinal cord";  
 RL J. Biol. Chem. 262:542-545(1987).  
 RN (9)  
 RP SEQUENCE OF 83-108, AND FUNCTION.  
 RC TISSUE=Phaeochromocytoma;  
 RX MEDLINE=92287083; PubMed=1318039;  
 RA Kitamura K., Kangawa K., Kawamoto M., Ichiki Y., Matsuo H., Eto T.;  
 RT "Isolation and characterization of peptides which act on rat  
 RT platelets, from a phaeochromocytoma";  
 RL Biochem. Biophys. Res. Commun. 185:134-141(1992).  
 RN (10)  
 RP STRUCTURE BY NMR OF CGRP.  
 RX MEDLINE=91105142; PubMed=1988044;  
 RA Breeze A.L., Harvey T.S., Bazzo R., Campbell I.D.;  
 RT "Solution structure of human calcitonin gene-related peptide by 1H  
 RT NMR and distance geometry with restrained molecular dynamics";  
 RL Biochemistry 30:575-582(1991).  
 RN (11)  
 RP STRUCTURE BY NMR OF CGRP.  
 RX MEDLINE=91248117; PubMed=2039456;  
 RA Hubbard J.A.M., Martin S.R., Chaplin L.C., Bose C., Kelly S.M.,  
 RA Price N.C.;  
 RT "Solution structures of calcitonin-gene-related-peptide analogues of  
 RT calcitonin-gene-related peptide and amylin";  
 RL Biochem. J. 275:785-788(1991).  
 CC -1- FUNCTION: CGRP induces vasodilatation. It dilates a variety of



vessels including the coronary, cerebral and systemic vasculature. Its abundance in the CNS also points toward a neurotransmitter or neuromodulator role. It also elevates platelet CAMP.

-1- ALTERNATIVE PRODUCTS: 3 ISOCORNS: 1 (AC P01258), 2 (AC P01258) AND 3 (SHOWN HERE); ARE PRODUCED BY ALTERNATIVE SPLICING.

-1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

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DR EMBL; X15943; CAA34070.1; -  
 DR EMBL; X02330; CAA26190.1; -  
 DR EMBL; M12667; AAA51914.1; -  
 DR EMBL; M12664; AAA51914.1; JOINED.  
 DR EMBL; M12665; AAA51914.1; JOINED.  
 DR EMBL; K03512; AAA52011.1; -  
 DR EMBL; M28637; AAA52012.1; -  
 DR EMBL; M26094; AAA51912.1; -  
 DR PIR; B22716; TCHOR.  
 DR PIR; A22949; A22949.  
 DR PIR; A26142; A26142.  
 DR PIR; S07644; S07644.  
 DR MIM; I14130; -  
 DR InterPro; IPR001693; Calc\_CGRP\_IAPP.  
 DR InterPro; IPR002163; Calcitonin\_beta.  
 DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
 DR PRINTS; PR00817; CALCITONINB.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; 1.  
 DR Cleavage on pair of basic residues; Amidation; Alternative splicing;  
 KM Hormone: Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT PROPEP 26 80  
 FT PEPTIDE 83 119 CALCITONIN GENE-RELATED PEPTIDE 1.  
 FT PROPEP 125 128  
 FT DISULFID 84 89  
 FT MOD\_RES 119 119 AMIDATION (G-120 PROVIDE AMIDE GROUP).  
 FT CONFLICT 48 48 R -> V (IN REF. 4).  
 FT CONFLICT 76 76 R -> V (IN REF. 3).  
 FT SEQUENCE 128 AA; 13899 MW; A003A106926DD9B8 CRC64;

Query Match 85.7%; Score 128.5; DB 1; Length 128;  
 Best Local Similarity 90.0%; Pred. No. 1.9e-12;  
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNGSKAF 30  
 DB 91 THRLAGLSRSGGVKNNF-VPTNGSKAF 119

RESULT 3  
 CGRP\_SHEEP STANDARD; PRT; 37 AA.  
 AC P30881;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 15-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Calcitonin gene-related peptide (CGRP).  
 OS Ovis aries (Sheep).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidae;  
 CC Bovidae; Caprinae; Ovis.  
 OC NCBI\_Taxid=9940;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=93038624; PubMed=1417824;

RA Miyata A., Jiang L., Minamino N., Arimura A.;  
 RT "Identification of calcitonin gene related peptide in ovine  
 RT hypothalamic extract."  
 RL Biochem. Biophys. Res. Commun. 187:1474-1479(1992).  
 CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF  
 CC VESSELS INCLUDING THE CORONARY, CEREAL AND SYSTEMIC VASCULATURE.  
 CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR  
 CC NEUROMODULATOR ROLE.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC PIR; JH0709; JH0709.  
 DR InterPro; IPR001693; Calc\_CGRP\_IAPP.  
 DR InterPro; IPR002163; Calcitonin\_beta.  
 DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
 DR PRINTS; PR00817; CALCITONINB.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; 1.  
 DR Amidation; hormone.  
 FT DISULFID 2 7  
 FT MOD\_RES 37 37 BY SIMILARITY.  
 FT SEQUENCE 37 AA; 3780 MW; F5DD64D248B6A47 CRC64;

Query Match 85.0%; Score 127.5; DB 1; Length 37;  
 Best Local Similarity 90.0%; Pred. No. 7.4e-13;  
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNGSKAF 30  
 DB 9 THRLAGLSRSGGVKSNF-VPTNGSQAF 37

RESULT 4  
 ID CGRP\_PIG STANDARD; PRT; 37 AA.  
 AC P30880;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Calcitonin gene-related peptide (CGRP).  
 OS Sus scrofa (Pig).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_Taxid=9823;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=87173481; PubMed=3494209;  
 RA Kimura S., Sugita Y., Kanazawa I., Saito A., Goto K.;  
 RT "Isolation and amino acid sequence of calcitonin gene related peptide  
 RT from porcine spinal cord."  
 RL Neuropeptides 9:75-82(1987).  
 CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF  
 CC VESSELS INCLUDING THE CORONARY, CEREAL AND SYSTEMIC VASCULATURE.  
 CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR  
 CC NEUROMODULATOR ROLE.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 DR InterPro; IPR001693; Calc\_CGRP\_IAPP.  
 DR InterPro; IPR002163; Calcitonin\_beta.  
 DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
 DR PRINTS; PR00817; CALCITONINB.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; 1.  
 DR Amidation; hormone.  
 FT DISULFID 2 7 BY SIMILARITY.  
 FT MOD\_RES 37 37 AMIDATION.  
 FT SEQUENCE 37 AA; 3814 MW; 04CDEB8D248B64BA CRC64;

Query Match 84.3%; Score 126.5; DB 1; Length 37;  
 Best Local Similarity 90.0%; Pred. No. 1.1e-12;  
 Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGVKSNFVPTNGSKAF 30  
 DB 1 THRLAGLSRSGGVKSNF-VPTNGSKAF 119

DB 9 THRLAGLSRSGWVKNF-VPTDVGSEAF 37

RESULT 5

AC CAL1\_RAT STANDARD; PRT; 128 AA.

AC P01256;

DT 21-JUL-1986 (Rel. 01, Created)

DT 01-APR-1988 (Rel. 07, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcitonin gene-related peptide I precursor (CGRP-I) (Alpha-type CGRP).

GN CALCA OR CALC.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85166259; PubMed=3872459;

RA Jonas V., Lin C.R., Kawashima E., Semon D., Swanson L.W., Mermod J.-J., Evans R.M., Rosenfeld M.G.;

RT "Alternative RNA processing events in human calcitonin/calcitonin gene-related peptide gene expression."

RL Proc. Natl. Acad. Sci. U.S.A. 82:1994-1998(1985).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=82220111; PubMed=6283379;

RA Amara S.G., Jones V., Rosenfeld M.G., Ong E.S., Evans R.M.;

RT "Alternative RNA processing in calcitonin gene expression generates mRNAs encoding different polypeptide products."

RL Nature 296:240-244(1982).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=85300490; PubMed=2994212;

RA Amara S.G., Arizka J.L., Leff S.E., Swanson L.W., Evans R.M., Rosenfeld M.G.;

RT "Expression in brain of a messenger RNA encoding a novel neuropeptide homologous to calcitonin gene-related peptide."

RL Science 229:1094-1097(1985).

CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE. ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR NEUROMODULATOR ROLE.

CC -1- ALTERNATIVE PRODUCTS: THE CALCITONIN PRECURSOR AND THE CALCITONIN RELATED PEPTIDE PRECURSOR ARE OBTAINED BY TISSUE-SPECIFIC SPLICING OF THE SAME GENE.

CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

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CC -----

DR EMBL; L29188; AAB59682.1; -

DR EMBL; L00109; AAB59682.1; JOINED.

DR EMBL; L00110; AAB59682.1; JOINED.

DR EMBL; V01231; CAA24541.1; -

DR EMBL; M1597; AAA40847.1; -

DR PIR; A01524; TCRTR.

DR PIR; B22949; B22949.

DR InterPro; IPR001693; Calc\_CGRP\_IAPP.

DR InterPro; IPR002163; Calcitonin\_beta.

DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.

DR PRINTS; PR00817; CALCITONINB.

DR SMART; SM00113; CALCITONINB.

DR PROSITE; PS00258; CALCITONIN; 1.

DR Cleavage on pair of basic residues; Amidation; Alternative splicing; Hormone; Signal.

FT SIGNAL 1 25

FT PROPEP 26 80

FT PEPTIDE 83 119

FT PROPEP 125 128

FT DISULFID 84 89

FT MOD\_RES 119 119

FT CONFLICT 40 40

FT CONFLICT 51 51

FT CONFLICT 70 70

FT CONFLICT 99 99

SO SEQUENCE 128 AA; 13948 MW; 75D14869C17078D3 CRC64;

Query Match 82.3%; Score 123.5; DB 1; Length 128;

Best Local Similarity 86.7%; Pred. No. 1,1e-11;

Matches 26; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGWVKNFVPTDVGSEAF 30

DB 91 THRLAGLSRSGWVKNF-VPTDVGSEAF 119

RESULT 6

AC CAL2\_RAT STANDARD; PRT; 134 AA.

AC P10093;

DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Calcitonin gene-related peptide II precursor (CGRP-II) (Beta-type CGRP).

GN CALC9.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=85300490; PubMed=2994212;

RA Amara S.G., Arizka J.L., Leff S.E., Swanson L.W., Evans R.M., Rosenfeld M.G.;

RT "Expression in brain of a messenger RNA encoding a novel neuropeptide homologous to calcitonin gene-related peptide."

RL Science 229:1094-1097(1985).

CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE. ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR NEUROMODULATOR ROLE.

CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.

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CC -----

DR EMBL; M1596; AAA40850.1; -

DR PIR; A44173; A44173.

DR InterPro; IPR001693; Calc\_CGRP\_IAPP.

DR InterPro; IPR002163; Calcitonin\_beta.

DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.

DR PRINTS; PR00817; CALCITONINB.

DR SMART; SM00113; CALCITONINB.

DR PROSITE; PS00258; CALCITONIN; 1.

DR Cleavage on pair of basic residues; Amidation; Hormone; Signal.

FT SIGNAL 1 26

FT PROPEP 27 86

FT PEPTIDE 89 125

FT PROPEP 131 134

FT DISULFID 90 95

FT MOD\_RES 125 125

SO SEQUENCE 134 AA; 14965 MW; BF6CAFB87A489B38 CRC64;

BY SIMILARITY.

AMIDATION (G-126 PROVIDE AMIDE GROUP).

AMIDATION (G-126 PROVIDE AMIDE GROUP).

[illegible]

AC P81564;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE Skin calcitonin gene-related peptide precursor (S-CGRP).  
 OS Phylomedusa bicolor (Two-colored leaf frog).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Amphibia; Batrachia; Anura; Neobatrachia; Bufonidae; Hylidae;  
 CC Phylomedusa.  
 CC NCBI\_Taxid=8393;  
 RN [1]  
 RP SEQUENCE FROM N.A., SEQUENCE OF 70-106, AND CHARACTERIZATION.  
 RC TISSUE-SKIN;  
 RX MEDLINE=20148807; PubMed=10681586;  
 RA Seon A.A., Pierre T.N., Redeker V., Lacombe C., Delfour A.,  
 RA Nicolas P., Amiche M.;  
 RT "Isolation, structure, synthesis, and activity of a new member of the  
 RT calcitonin gene-related peptide family from frog skin and molecular  
 RT cloning of its precursor".  
 RL J. Biol. Chem. 275:5934-5940(2000).  
 CC -1- FUNCTION: CGRP INDUCES VASODILATION. IT DILATES A VARIETY OF  
 CC VESSELS INCLUDING THE CORONARY, CEREBRAL AND SYSTEMIC VASCULATURE.  
 CC ITS ABUNDANCE IN THE CNS ALSO POINTS TOWARD A NEUROTRANSMITTER OR  
 CC NEUROMODULATOR ROLE (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: SKIN, INTERSTINE AND BRAIN.  
 CC -1- MASS SPECTROMETRY: MW=3.806.77; METHOD=MALDI; RANGE=70-106.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; Y18495; CAB76385.1; -  
 DR InterPro: IPR001693; Calc\_CGRP\_IAPP.  
 DR InterPro: IPR002163; Calcitonin\_beta.  
 DR Pfam: PF00214; Calc\_CGRP\_IAPP; 1.  
 DR PRINTS: PR00817; CALCITONINB.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; 1.  
 KW Signal; Cleavage on pair of basic residues; Amidation; Hormone;  
 KW Amphibian skin.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT PROPEP 26 69 REMOVED IN MATURE FORM BY  
 FT CHAIN 70 106 CARBOXYPEPTIDASE.  
 FT PROPEP 107 115 SKIN CALCITONIN GENE-RELATED PEPTIDE.  
 FT DISULF 71 76 REMOVED IN MATURE FORM BY ENDOPROTEASE.  
 FT MOD\_RES 106 106 AMIDATION (G-107 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 115 AA: 12438 MW: 453D11255CA53D31 CRC64;

Query Match 45.7%; Score 68.5; DB 1; Length 115;  
 Best Local Similarity 53.3%; Pred. No. 0.0021;  
 Matches 16; Conservative 5; Mismatches 8; Indels 1; Gaps 1;

OY 1 HRLAGLSRSGGMVKNFVPTNGSKAF 30  
 DB 78 TORLADFLSRSGIGSPDF-VPTDVSANSF 106

RESULT 10  
 IAPP\_SAGE STANDARD; PRT; 32 AA.  
 AC Q28934;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Islet amyloid polypeptide (Amylin) (Fragment).  
 DE

GN IAPP.  
 OS Saginus oedipus (Cotton-top tamarin).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Saginus.  
 CC NCBI\_Taxid=9490;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Albrandt K., Sierzege M.E., Mull E., Brady E.M.G.;  
 RL Submitted (Aug-1996) to the EMBL/Genbank/DBP databases.  
 CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE  
 CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING  
 CC ADIPOCYTE GLUCOSE METABOLISM.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; U62627; AAB05918.1; -  
 DR InterPro: IPR001693; Calc\_CGRP\_IAPP.  
 DR Pfam; PF00214; Calc\_CGRP\_IAPP; 1.  
 DR SMART; SM00113; CALCITONIN; 1.  
 DR PROSITE; PS00258; CALCITONIN; PARTIAL.  
 KW Hormone; Amyloid.  
 FT NON\_TER 1 1  
 FT PEPTIDE <1 >32 ISLET AMYLOID POLYPEPTIDE.  
 FT NON\_TER 32 32  
 SQ SEQUENCE 32 AA: 3340 MW: 91A219AE3882C02 CRC64;

Query Match 35.7%; Score 53.5; DB 1; Length 32;  
 Best Local Similarity 51.7%; Pred. No. 0.1;  
 Matches 15; Conservative 2; Mismatches 5; Indels 7; Gaps 2;

OY 2 HRLAGLSRSGGMVKNF--VYPTNGS 27  
 DB 8 HRLADFLGRS----SNNFGALISPTNGS 32

RESULT 11  
 PA2D\_MOUSE STANDARD; PRT; 144 AA.  
 AC Q9WVF6; Q9JLK0;  
 DT 01-MAR-2002 (Rel. 41, Created)  
 DT 01-MAR-2002 (Rel. 41, Last sequence update)  
 DE Group IID secretory phospholipase A2 precursor (EC 3.1.1.4)  
 DE (Phosphatidylcholine 2-acylhydrolase GII) (GII sPLA2) (PLA2IID)  
 DE (sPLA2-IIID) (Secretory-type PLA, stroma-associated homolog).  
 GN PLA2G2D OR PLA2A2 OR SPLASH.  
 OS Mus musculus (mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 CC NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.  
 RC STRATIN-BALB/C;  
 RX MEDLINE=99386983; PubMed=10455175;  
 RA Ishizaki J., Suzuki N., Higashino K.-I., Yokota Y., Ono T.,  
 RA Kawamoto K., Fujii N., Arita H., Hanasaki K.;  
 RT Cloning and characterization of novel mouse and human secretory  
 RT phospholipase A2s".  
 RL J. Biol. Chem. 274:24973-24979(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RX MEDLINE=99315857; PubMed=10383420;  
 RA Valentin E., Koduri R.S., Scimeca J.-C., Carle G., Gelb M.H.,  
 RA Lazdunski M., Lambeau G.;  
 RT Cloning and recombinant expression of a novel mouse-secreted

RT phospholipase A2.";  
 RL J. Biol. Chem. 274:19152-19160(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN-129 X C57BL/6;  
 RX MEDLINE-21040292; PubMed-11196711;  
 RA Shakhov A.N., Rubtsov A.V., Lyakhov I.G., Tumanov A.V.,  
 Nedospasov S.A.;  
 RT "SPLASH (PLA(2)IID), a novel member of phospholipase A2 family, is  
 RL associated with lymphotoxin deficiency.";  
 genes Immun. 1:191-199(2000).  
 [4]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC STRAIN-C57BL/6J; TISSUE=Thymus;  
 RX MEDLINE-21085660; PubMed-11217851;  
 RA Kawai J., Shingawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 Atkawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 Alawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 Fleischmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 Schiraldi L.M., Staudt F., Suzuki K., Tomita M., Wagner L., Washio T.,  
 Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
 Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,  
 Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-  
 CC acyl groups in 3-sn-phosphoglycerides. L-alpha-1-palmitoyl-2-  
 CC 1-lycophosphatidylethanolamine is more efficiently hydrolyzed  
 CC than the other phospholipids examined.  
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-  
 CC acylglycerophosphocholine + a fatty acid anion.  
 CC -1- COFACTOR: Binds 1 calcium ion per subunit.  
 CC -1- SUBCELLULAR LOCATION: Secreted (isoform 1) and Cytoplasmic  
 CC (isoform 2) (Potential).  
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms: 1 (shown here) and 2; are  
 CC produced by alternative splicing.  
 CC -1- TISSUE SPECIFICITY: Expressed in several tissues including  
 CC pancreas, spleen, thymus, skin, lung, and ovary.  
 CC -1- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.  
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 CC -----  
 DR EMBL: AF112983; AAD51391.1; -  
 DR EMBL: AF124374; AAD42773.1; -  
 DR EMBL: AF188624; AAF09019.1; -  
 DR EMBL: AF169407; AAF42987.1; -  
 DR EMBL: AF169408; AAF42988.1; -  
 DR EMBL: AK018005; BAB31033.1; -  
 DR EMBL: AK004232; BAB3230.1; -  
 DR HSSP: P24605; 1CLP.  
 DR MGD: MGI:1341796; Plaz29d.  
 DR InterPro: IPR001211; PLP\_A2.  
 DR Pfam: PF00068; phoslip; 1.  
 DR PRINTS: PR00389; PHPLIPASEA2.  
 DR ProDom: PD00303; PLP\_A2; 1.  
 DR SMART: SM00085; PA2c; 1.  
 DR PROSITE: PS00119; PA2\_ASP; 1.

DR PROSITE: PS00118; PA2\_HIS; 1.  
 KW Hydrolase; Lipid degradation; Signal; Calcium; Alternative splicing.  
 FT SIGNAL 1 19  
 FT CHAIN 20 144  
 FT ACT\_SITE 66 66  
 FT ACT\_SITE 111 111  
 FT ACT\_SITE 45 137  
 FT DISULFID 47 63  
 FT DISULFID 62 117  
 FT DISULFID 68 144  
 FT DISULFID 69 110  
 FT DISULFID 78 103  
 FT DISULFID 96 108  
 FT CARBOHYD 99 99  
 FT CA\_BIND 46 46  
 FT CA\_BIND 48 48  
 FT CA\_BIND 50 50  
 FT CA\_BIND 67 67  
 FT VARSPIC 1 26  
 SQ SEQUENCE 144 AA; 16164 MW; 7697ADA07F8D270A CRC64;  
 Query Match 34.7%; Score 52; DB 1; Length 144;  
 Best Local Similarity 40.7%; Pred. No. 0.83;  
 Matches 11; Conservative 5; Mismatches 11; Indels 0; Gaps 0;  
 Oy 4 LAGLSRSGGMVKSFPVPTNGSKAF 30  
 Db 11 LAGITATGGLMLNKNMVTHTMCKKAF 37  
 RESULT 12  
 IAPP\_FELCA STANDARD; PRT; 89 AA.  
 AC P12967;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 01-NOV-1995 (Rel. 32, Last annotation update)  
 DE Islet amyloid polypeptide precursor (Amylin).  
 GN IAPP.  
 OS Felis silvestris catus (Cat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.  
 OX NCBI\_TaxID=9685;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-89345542; PubMed-2668946;  
 RA Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.;  
 RT "Conservation of the sequence of islet amyloid polypeptide in five  
 RT mammals is consistent with its putative role as an islet hormone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).  
 [2]  
 RP SEQUENCE OF 34-50.  
 RX MEDLINE-87231921; PubMed-3035556;  
 RA Westermarck P., Wernstedt C., Wlinder E., Hayden D.W., O'Brien T.D.,  
 RA Johnson K.H.;  
 RT "Amyloid fibrils in human insulinoma and islets of Langerhans of the  
 RT diabetic cat are derived from a neuropeptide-like protein also  
 RT present in normal islet cells.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3881-3885(1987).  
 CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE  
 CC UTILIZATION AND GLYCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING  
 CC ADIPOCYTE GLUCOSE METABOLISM.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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DR EMBL: M25388; AAA30813.1; -  
 DR PIR: A33542; A33542.  
 DR PIR: B26619; B26619.  
 DR InterPro: IPR001693; Calc\_CGRP\_TAPP.  
 DR InterPro: IPR000443; Islet\_Amyloid.  
 DR Pfam: PF00214; Calc\_CGRP\_TAPP; 1.  
 DR PRINTS: PR00818; ISLETAMYLOID.  
 DR SMART: SM00113; CALCITONIN; 1.  
 DR PROSITE: PS00258; CALCITONIN; 1.  
 DR Hormone: Cleavage on pair of basic residues; Amidation; Amyloid;  
 KW Signal.  
 FT SIGNAL 1 22 POTENTIAL.  
 FT PEPTIDE 34 70 ISLET AMYLOID POLYPEPTIDE.  
 FT DISULFID 35 40 BY SIMILARITY.  
 FT MOD\_RES 70 70 AMIDATION (G-71 PROVIDE AMIDE GROUP).  
 SQ SEQUENCE 89 AA: 9831 MW: 0834D783DEAD72A8 CRC64;

Query Match 33.7%; Score 50.5; DB 1; Length 89;  
 Best Local Similarity 43.3%; Pred. No. 0.85;  
 Matches 13; Conservative 4; Mismatches 12; Indels 1; Gaps 1;

Oy 1 THRLAGLLSRSGMKSNFVPTVNGSKAF 30  
 Db 42 TORLANFLIRSSNNLGA-TLSPVNGSNFY 70

RESULT 13  
 FMQ MORBO STANDARD; PRT; 157 AA.  
 AC P07640;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Fibrital protein Q precursor (Beta p11n) (Q p11n).  
 GN TFPO.  
 OS Moraxella bovis.  
 OC Bacteria; Proteobacteria; gamma subdivision; Moraxellaceae; Moraxella.  
 OX NCBI\_TaxID=476;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EPP63;  
 RX MEDLINE=85234350; PubMed=2861194;  
 RA Marrs C.F., Schoolnik G., Koomey J.M., Hardy J., Rothbard J.,  
 RA Falkow S.;  
 RT "Cloning and sequencing of a Moraxella bovis p11n gene";  
 RL J. Bacteriol. 163:132-139(1985).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EPP63;  
 RX MEDLINE=90094235; PubMed=2403542;  
 RA Fuiks K.A., Marrs C.F., Stevens S.P., Green M.R.;  
 RT "Sequence analysis of the inversion region containing the p11n genes  
 RT of Moraxella bovis";  
 RL J. Bacteriol. 172:310-316(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=91286182; PubMed=2061282;  
 RA Roza F.W., Marrs C.F.;  
 RT "Interesting sequence differences between the p11n gene inversion  
 RT regions of Moraxella lacunata ATCC 17956 and Moraxella bovis Epp63";  
 RL J. Bacteriol. 173:4000-4006(1991).  
 RN [4]  
 RP SEQUENCE OF 7-157.  
 RX MEDLINE=89010522; PubMed=2902184;  
 RA Ruehl W.W., Marrs C.F., Fernandez R., Falkow S., Schoolnik G.K.;  
 RT "Purification, characterization, and pathogenicity of Moraxella bovis  
 RT p11n";  
 RL J. Exp. Med. 168:983-1002(1988).  
 CC -1- SUBUNIT: THE P11N ARE POLAR FLEXIBLE FILAMENTS OF ABOUT 5.4  
 CC NANOMETERS DIAMETER AND 2.5 MICROMETERS AVERAGE LENGTH; THEY  
 CC CONSIST OF ONLY A SINGLE POLYPEPTIDE CHAIN ARRANGED IN A HELICAL  
 CC CONFIGURATION OF FIVE SUBUNITS PER TURN IN THE ASSEMBLED FILUS.

CC -1- MISCELLANEOUS: MORAXELLA BOVIS CAN EXPRESS EITHER A Q OR A I  
 CC PILIN, THE INVERSION OF 2 KB OF DNA DETERMINES WHICH PILIN IS  
 CC EXPRESSED.  
 CC -1- SIMILARITY: BELONGS TO THE N-ME-PHE PILI FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M1435; AAA25304.1; -  
 DR EMBL: M32345; AAA88223.1; -  
 DR EMBL: M59712; AAA825308.1; -  
 DR PIR: A24434; A24434.  
 DR PIR: J10072; J10072.  
 DR InterPro: IPR001082; P11n.  
 DR InterPro: IPR001120; Prok\_N\_methyltn.  
 DR Pfam: PF00114; p11n; 1.  
 DR PRODOM: PD000666; P11n; 1.  
 DR PROSITE: PS00409; PROKAR\_NTER\_METHYL; 1.  
 KW Fibrital; Methylation.  
 FT PROPEP 1 6 FIBRITAL PROTEIN Q.  
 FT CHAIN 7 157 METHYLATION.  
 FT MOD\_RES 7 7 BY SIMILARITY.  
 FT DISULFID 136 155  
 SQ SEQUENCE 157 AA: 16006 MW: A923CD8A26C693C9 CRC64;

Query Match 32.7%; Score 49; DB 1; Length 157;  
 Best Local Similarity 39.1%; Pred. No. 2.6;  
 Matches 9; Conservative 5; Mismatches 9; Indels 0; Gaps 0;

Oy 8 LSRSGMKSNFVPTVNGSKAF 30  
 Db 78 LTTTGCTARSNNLMSVNIIGGAF 100

RESULT 14  
 GUXL PHACH STANDARD; PRT; 516 AA.  
 ID GUXL PHACH  
 AC P13860;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Exoglucanase I precursor (EC 3.2.1.91) (Exocellobiohydrolase I)  
 DE (1,4-beta-cellobiohydrolase).  
 GN CBH1.  
 OS Phanerochaete chrysosporium.  
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;  
 OC Aphyllophorales; Corticiaceae; Phanerochaete.  
 OX NCBI\_TaxID=5306;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;  
 RX MEDLINE=89232732; PubMed=3246351;  
 RA Sims P.F.G., James C., Broda P.;  
 RT "The identification, molecular cloning and characterisation of a gene  
 RT from Phanerochaete chrysosporium that shows strong homology to the  
 RT exo-cellobiohydrolase I gene from Trichoderma reesei";  
 RL Gene 74:411-422(1988).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ME446;  
 RX MEDLINE=94335641; PubMed=8057846;  
 RA Sims P.F.G., Soares-Felipe M.S., Wang Q., Gent M.E., Tempelaars C.,  
 RA Broda P.;  
 RT "Differential expression of multiple exo-cellobiohydrolase I-like  
 RT genes in the lignin-degrading fungus Phanerochaete chrysosporium";  
 RL Mol. Microbiol. 12:209-216(1994).  
 CC -1- FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE

CC GENERALY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:  
 CC (1) ENDOGALACTOSIDASES WHICH CUT INTERNAL BETA-1,4-GLUCOSIDIC BONDS;  
 CC (2) EXOCELLULOBIOTRANSFERASES THAT CUT THE CELLULOSE POLYMER CHAIN;  
 CC FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;  
 CC (3) BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLULOSE AND OTHER  
 CC SHORT CELLULO-OLIGOSACCHARIDES TO GLUCOSE.  
 CC CATALYTIC ACTIVITY: Hydrolysis of 1,4-beta-D-glucosidic linkages  
 CC in cellulose and cellotriose, releasing cellobiose from the non-  
 CC reducing ends of the chains.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO CELLULOSE FAMILY C (FAMILY 7 OF GLYCOSYL  
 CC HYDROLASES).  
 CC -1- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBR).  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M22220; AAB46373.1; -;  
 CC EMBL: Z22228; CA80253.1; -;  
 CC PIR: JS0083; JS0083.  
 CC HSP: P00725; 2CBH.  
 CC InterPro: IPR000254; Glyco\_hydro\_7.  
 CC InterPro: IPR001722; Glyco\_hydro\_7.  
 CC Pfam: PF00734; CBD\_1; 1.  
 CC Pfam: PF00840; Glyco\_hydro\_7; 1.  
 CC PRINTS: PR00734; GLHYDRLASE7.  
 CC ProDom: PD001821; CBD\_fungal; 1.  
 CC ProDom: PD186135; Glyco\_hydro\_7; 1.  
 CC SMART: SM00236; fcbd\_1.  
 CC PROSITE: PS00562; CBD\_FUNGAL; 1.  
 CC Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.  
 CC FM SIGNAL 1 18  
 CC FT CHAIN 19 516  
 CC FT DOMAIN ? 449  
 CC FT DOMAIN 450 480  
 CC FT DOMAIN 481 516  
 CC FT ACT\_SITE 225 225  
 CC FT ACT\_SITE 230 230  
 CC FT CARBOHYD 208 208  
 CC FT CARBOHYD 326 326  
 CC FT CARBOHYD 442 442  
 CC FT DISULFID 488 505  
 CC FT DISULFID 499 515  
 CC FT DISULFID 27 28  
 CC FT CONFLICT 30 31  
 CC FT CONFLICT 31 31  
 CC SEQUENCE 516 AA; 54857 MW; 1C7C3D338ECE1B72 CRC64;  
 SO  
 Query Match 32.7%; Score 49; DB 1; Length 516;  
 Best Local Similarity 39.1%; Pred. No. 8.9;  
 Matches 9; Conservative 6; Mismatches 8; Indels 0; Gaps 0;  
 Oy 8 LSRSGMVKNSFVPTNGSKAF 30  
 Db 102 ITASGSSLKLPFTGNSVNGSRV 124  
 RESULT 15  
 IAPP\_MOUSE STANDARD; PRT; 93 AA.  
 AC P12968;  
 DT 01-OCT-1989 (Rel. 12, Created)  
 DT 01-OCT-1989 (Rel. 12, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE Islet amyloid polypeptide precursor (Diabetes-associated peptide)  
 DE (DAP) (Amylin).  
 GN IAPP.  
 OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=8934542; PubMed=2668946;  
 RA Nishi M., Chan S.J., Nagamatsu S., Bell G.I., Steiner D.F.;  
 RT "Conservation of the sequence of islet amyloid polypeptide in five  
 RT mammals is consistent with its putative role as an islet hormone.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:5738-5742(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BA/2J; TISSUE=Liver;  
 RA MEDLINE=97424750; PubMed=9278663;  
 RX Ekwa K., Nishi M., Ohagi S., Sanke T., Nanjo K.;  
 RT "Cloning of mouse islet amyloid polypeptide gene and characterization  
 RT of its promoter.";  
 RL J. Mol. Endocrinol. 19:79-86(1997).  
 RN [3]  
 RP SEQUENCE OF 38-74.  
 RX MEDLINE=89325677; PubMed=2666169;  
 RA Betsholtz C., Christmansson L., Engstrom U., Rorsman F., Svensson V.,  
 RA Johnson K.H., Westermark P.;  
 RT "Sequence divergence in a specific region of islet amyloid  
 RT polypeptide (IAPP) explains differences in islet amyloid formation  
 RT between species.";  
 RL FEBS Lett. 251:261-264(1989).  
 CC -1- FUNCTION: SELECTIVELY INHIBITS INSULIN-STIMULATED GLUCOSE  
 CC UTILIZATION AND GLUCOGEN DEPOSITION IN MUSCLE, WHILE NOT AFFECTING  
 CC ADIPOCYTE GLUCOSE METABOLISM.  
 CC -1- SIMILARITY: BELONGS TO THE CALCITONIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: M25389; AAA37874.1; -;  
 CC EMBL: D31820; BAA22051.1; -;  
 CC EMBL: D31819; BAA22051.1; JOINED.  
 CC PIR: S05039; S05039.  
 CC PIR: C33542; C33542.  
 CC MGD: MG1:96382; IAPP.  
 CC InterPro: IPR001693; Calc\_CGRP\_IAPP.  
 CC InterPro: IPR000443; Islet\_amyloid.  
 CC Pfam: PF00214; Calc\_CGRP\_IAPP; 1.  
 CC PRINTS: PR00818; ISLETAMYLID.  
 CC SMART: SM00113; CALCITONIN; 1.  
 CC PROSITE: PS00258; CALCITONIN; 1.  
 CC Hormone; Cleavage on pair of basic residues; Amidation; Amyloid;  
 CC FM SIGNAL 1 23  
 CC FT PEPTIDE 38 74  
 CC FT DISULFID 39 74  
 CC FT MOD\_RES 74 74  
 CC SEQUENCE 93 AA; 10022 MW; B135DBC81475B15 CRC64;  
 SO  
 Query Match 32.3%; Score 48.5; DB 1; Length 93;  
 Best Local Similarity 43.3%; Pred. No. 1.8;  
 Matches 13; Conservative 3; Mismatches 13; Indels 1; Gaps 1;  
 Oy 1 THRLAGLSRSGMVKNSFVPTNGSKAF 30  
 Db 46 TÖRLANFLVRSSNNL-GVPLPTNGSNTY 74

Search completed: August 26, 2002, 15:53:25  
 Job time: 121 sec

[Illegible text]

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 26, 2002, 15:49:48 ; Search time 12.97 Seconds  
(without alignments)  
56.497 Million cell updates/sec

Title: US-09-813-345-2

Perfect score: 150  
Sequence: 1 THRLAGLSRSGMWKSNFYPTNGSKAF 30

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

1: Issued\_Patents\_AA:\*  
2: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep:\*  
3: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep:\*  
4: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep:\*  
5: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep:\*  
6: /cgn2\_6/ptodata/2/1aa/Backfilltest.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	% Query Match	Length	ID	Description
1	150	100.0	30	4	US-09-070-504-2
2	135.5	90.3	29	4	US-09-070-504-1
3	135.5	90.3	37	1	US-08-233-389C-9
4	135.5	90.3	37	2	US-08-801-863-9
5	135.5	90.3	37	2	US-08-486-596A-9
6	135.5	90.3	37	2	US-09-004-713-9
7	135.5	90.3	37	2	US-08-619-841-2
8	135.5	90.3	37	2	US-08-446-929A-2
9	135.5	90.3	37	4	US-09-070-504-3
10	135.5	90.3	38	1	US-07-776-272-20
11	131.5	87.7	37	4	US-09-070-504-8
12	128.5	85.7	29	1	US-07-794-288D-26
13	128.5	85.7	30	2	US-07-794-288D-27
14	128.5	85.7	35	1	US-08-460-890A-45
15	128.5	85.7	35	3	US-08-167-641C-45
16	128.5	85.7	35	4	US-08-462-040-45
17	128.5	85.7	35	4	US-08-462-040-45
18	128.5	85.7	37	1	US-07-794-288D-3
19	128.5	85.7	37	1	US-08-233-389C-8
20	128.5	85.7	37	2	US-08-801-863-8
21	128.5	85.7	37	2	US-08-486-596A-8
22	128.5	85.7	37	2	US-09-004-713-8
23	128.5	85.7	37	2	US-08-619-841-1
24	128.5	85.7	37	2	US-08-446-929A-1
25	128.5	85.7	37	4	US-09-070-504-4
26	128.5	85.7	37	6	US-07-776-272-19
27	128.5	85.7	38	1	US-07-776-272-19

28	128.5	85.7	38	2	US-08-460-890A-44	Sequence 44, Appl
29	128.5	85.7	38	3	US-08-167-641C-44	Sequence 44, Appl
30	128.5	85.7	38	4	US-08-460-971A-44	Sequence 44, Appl
31	128.5	85.7	38	4	US-08-462-040-44	Sequence 44, Appl
32	127.5	85.0	37	4	US-09-070-504-5	Sequence 5, Appl
33	127.5	85.0	37	4	US-09-070-504-10	Sequence 10, Appl
34	127.5	85.0	37	4	US-09-070-504-11	Sequence 11, Appl
35	127.5	85.0	38	1	US-07-776-272-22	Sequence 22, Appl
36	126.5	84.3	37	4	US-09-070-504-9	Sequence 9, Appl
37	123.5	82.3	28	1	US-07-794-288D-28	Sequence 28, Appl
38	123.5	82.3	37	4	US-09-070-504-6	Sequence 6, Appl
39	123.5	82.3	38	1	US-07-776-272-21	Sequence 21, Appl
40	122.5	81.7	28	1	US-07-794-288D-127	Sequence 127, App
41	122.5	81.7	29	1	US-07-794-288D-72	Sequence 72, Appl
42	121.5	81.0	37	6	5424221-5	Patent No. 5424221
43	121	80.7	29	1	US-07-794-288D-96	Sequence 96, Appl
44	118.5	79.0	27	1	US-07-794-288D-128	Sequence 128, App
45	118.5	79.0	28	1	US-07-794-288D-73	Sequence 73, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-070-504-2
; Sequence 2, Application US/09070504
; Patent No. 6268474
GENERAL INFORMATION:
APPLICANT: Smith, Derek D.
APPLICANT: Sana, Shankar
APPLICANT: Abel, Peter W.
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESS: Moeling, Raasch & Gebhardt, P.A.
STREET: 119 No. 6268474th Fourth Street
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/070,504
FILING DATE: 30-Apr-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McCormick, Myra H
REGISTRATION NUMBER: 36,602
REFERENCE/DOCKET NUMBER: 180,00020101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612/305-1220
TELEFAX: 612/305-1228
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-070-504-2

Query Match 100.0%; Score 150; DB 4; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e-15;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 THRLAGLSRSGMWKSNFYPTNGSKAF 30
|||||
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DB 1 THRLAGLSRSGMWKSNFVPTNWSKAF 30

RESULT 2

US-09-070-504-1

Sequence 1, Application US/09070504

Patent No. 6268474

GENERAL INFORMATION:

APPLICANT: Smith, Derek D.

APPLICANT: Saha, Shankar

APPLICANT: Abel, Peter W.

TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR

TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE

NUMBER OF SEQUENCES: 23

CORRESPONDENCE ADDRESS:

ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.

STREET: 119 No. 6268474th Fourth Street

CITY: Minneapolis

STATE: MN

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/070,504

FILING DATE: 30-APR-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: McCormack, Myra H

REGISTRATION NUMBER: 36,602

REFERENCE/DOCKET NUMBER: 180.00020101

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612/305-1220

TELEFAX: 612/305-1228

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 29 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-070-504-1

Query Match 90.3%; Score 135.5; DB 4; Length 29;

Best Local Similarity 96.7%; Pred. No. 1.3e-13;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMWKSNFVPTNWSKAF 30

DB 1 THRLAGLSRSGMWKSNFVPTNWSKAF 29

RESULT 3

US-08-233-389C-9

Sequence 9, Application US/08233389C

Patent No. 5639855

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/O FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/233,389C

FILING DATE: 26-APR-1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY JR., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-233-389C-9

Query Match 90.3%; Score 135.5; DB 1; Length 37;

Best Local Similarity 96.7%; Pred. No. 1.7e-13;

Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMWKSNFVPTNWSKAF 30

DB 9 THRLAGLSRSGMWKSNFVPTNWSKAF 37

RESULT 4

US-08-801-863-9

Sequence 9, Application US/08801863

Patent No. 5830703

GENERAL INFORMATION:

APPLICANT: KITAMURA, Kazuo

APPLICANT: KANGAWA, Kenji

APPLICANT: MATSUO, Hisayuki

APPLICANT: ETO, Tanenao

TITLE OF INVENTION: ADRENOMEDULLIN

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: C/O FISH & NEAVE

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/801,863

FILING DATE: CONCURRENTLY HERewith

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: HALEY JR., James F.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: SHGN-5 DIV3

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 37 amino acids

TYPE: amino acid



ATTORNEY/AGENT INFORMATION:  
NAME: Hodgins, Daniel S.  
REGISTRATION NUMBER: 31,026  
REFERENCE/DOCKET NUMBER: UTSG:195\HOD  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 474-7577  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-619-841-2

Query Match 90.3%; Score 135.5; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 1.7e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMWKSNFVPTNWGSKAF 30  
DB 9 THRLAGLSRSGMWKSNF-VPTNWGSKAF 37

RESULT 8  
US-08-446-929A-2  
Sequence 2, Application US/08446929A  
Patent No. 5958877  
GENERAL INFORMATION:  
APPLICANT: Wimalawansa, Sunil J.  
TITLE OF INVENTION: A Method for Counteracting  
TITLE OF INVENTION: Vasospasms, Ischemia, Renal Failure, and Treating Male  
TITLE OF INVENTION: Impotence Using Calcitonin Gene Related Peptide  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Rosenblatt & Redano, P.C.  
STREET: One Greenway Plaza, Suite 500  
CITY: Houston  
STATE: Texas  
COUNTRY: U.S.A.  
ZIP: 77046-0103  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.5 inch, 1.0 Mb storage  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Macintosh 7.5.3  
SOFTWARE: Microsoft Word 6.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/446,929A  
FILING DATE: 18-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
ATTORNEY/AGENT INFORMATION:  
NAME: Mossman, David L.  
REGISTRATION NUMBER: 29,570  
REFERENCE/DOCKET NUMBER: LEOC-90  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 210/542-8339  
TELEFAX: 210/544-7201  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: n/a  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE:  
PUBLICATION INFORMATION:  
AUTHORS: Wimalawansa, Sunil J.  
TITLE: Calcitonin: Molecular Biology, Physiology,  
Title: Pathophysiology and its Therapeutic Uses

JOURNAL: Advances in Bone Regulatory Factors  
JOURNAL: Morphology, Biochemistry, Physiology and Pharmacology  
JOURNAL:  
VOLUME: n/a  
ISSUE: n/a  
PAGES: 121-160  
DATE: 1989  
US-08-446-929A-2

Query Match 90.3%; Score 135.5; DB 2; Length 37;  
Best Local Similarity 96.7%; Pred. No. 1.7e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMWKSNFVPTNWGSKAF 30  
DB 9 THRLAGLSRSGMWKSNF-VPTNWGSKAF 37

RESULT 9  
US-09-070-504-3  
Sequence 3, Application US/09070504  
Patent No. 6268474  
GENERAL INFORMATION:  
APPLICANT: Smith, Derek D.  
APPLICANT: Saha, Shankar  
APPLICANT: Abel, Peter W.  
TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR  
TITLE OF INVENTION: SUPERFAMILY AND METHODS OF USE  
NUMBER OF SEQUENCES: 23  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Mueitng, Raasch & Gebhardt, P.A.  
STREET: 119 No. 6268474th Fourth Street  
CITY: Minneapolis  
STATE: MN  
COUNTRY: USA  
ZIP: 55401  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/070,504  
FILING DATE: 30-APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: McCormack, Myra H.  
REGISTRATION NUMBER: 36,602  
REFERENCE/DOCKET NUMBER: 180.00020101  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612/305-1220  
TELEFAX: 612/305-1228  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 37 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-070-504-3

Query Match 90.3%; Score 135.5; DB 4; Length 37;  
Best Local Similarity 96.7%; Pred. No. 1.7e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGMWKSNFVPTNWGSKAF 30  
DB 9 THRLAGLSRSGMWKSNF-VPTNWGSKAF 37

RESULT 10

US-07-776-272-20  
; Sequence 20, Application US/07776272  
; Patent No. 5612454  
; GENERAL INFORMATION:  
; APPLICANT: Kaminuma, Toshihiko  
; APPLICANT: Iida, Toshi  
; APPLICANT: Tajima, Masahito  
; TITLE OF INVENTION: Process for Purification of Polypeptide  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Wegner, Cantor, Mueller & Player  
; STREET: 1233 20th St. N.W. P.O. Box 18218  
; CITY: Washington  
; STATE: District of Columbia  
; COUNTRY: United States of America  
; ZIP: 20036-8218  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/776,272  
; FILING DATE: 19911129  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Player, William E  
; REGISTRATION NUMBER: 31,409  
; REFERENCE/DOCKET NUMBER: P-450-23167  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-887-0400  
; TELEFAX: 202-887-0605  
; TELEX: 440706  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 38 amino acids  
; TYPE: AMINO ACID  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; HYPOTHEICAL: YES  
; ORIGINAL SOURCE:  
; ORGANISM: Human  
; US-07-776-272-20

Query Match 90.3%; Score 135.5; DB 1; Length 38;  
Best Local Similarity 96.7%; Pred. No. 1.8e-13;  
Matches 29; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWKSNFVPTNVGSKAF 30  
Db 9 THRLAGLSRSGGWKSNF-VPTNVGSKAF 37

RESULT 11  
US-09-070-504-8  
; Sequence 8, Application US/09070504  
; Patent No. 6268474  
; GENERAL INFORMATION:  
; APPLICANT: Smith, Derek D.  
; APPLICANT: Saha, Shankar  
; APPLICANT: Abel, Peter W.  
; TITLE OF INVENTION: PEPTIDE ANTAGONISTS OF CGRP-RECEPTOR  
; NUMBER OF SEQUENCES: 23  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Mueling, Raasch & Gebhardt, P.A.  
; STREET: 119 No. 6268474th Fourth Street  
; CITY: Minneapolis  
; STATE: MN  
; COUNTRY: USA  
; ZIP: 55401  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,504  
; FILING DATE: 30-Apr-1998  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: McCormack, Myra H  
; REGISTRATION NUMBER: 36,602  
; REFERENCE/DOCKET NUMBER: 180,00020101  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 612/305-1220  
; TELEFAX: 612/305-1228  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 37 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-070-504-8

Query Match 87.7%; Score 131.5; DB 4; Length 37;  
Best Local Similarity 93.3%; Pred. No. 6.8e-13;  
Matches 28; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

OY 1 THRLAGLSRSGGWKSNFVPTNVGSKAF 30  
Db 9 THRLAGLSRSGGWKSNF-VPTNVGSEAF 37

RESULT 12  
US-07-794-288D-27  
; Sequence 27, Application US/07794288D  
; Patent No. 5580953  
; GENERAL INFORMATION:  
; APPLICANT: ELISABETH ALBRECHT,  
; APPLICANT: HOWARD JONES,  
; APPLICANT: LAURA S.L. GAETA,  
; APPLICANT: KATHRYN S. PRICKETT and  
; APPLICANT: KEVIN BEAUMONT  
; TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
; NUMBER OF SEQUENCES: 227  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: LYON & LYON  
; STREET: First Interstate World  
; STREET: Center  
; STREET: 633 West Fifth Street,  
; STREET: Suite 4700  
; CITY: Los Angeles  
; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 90071-2066  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 3.5" Diskette, 1.44  
; MEDIUM TYPE: 5.25" Diskette, 1.44  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: IBM M.S. DOS (Version  
; SOFTWARE: WordPerfect (Version 5.1)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/07/794,288D  
; FILING DATE: Herewith  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/794,288  
; FILING DATE: 19-NOV-91  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Duft, Bradford, J.

REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 29 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-27

Query Match 85.7%; Score 128.5; DB 1; Length 29;  
Best Local Similarity 90.0%; Pred. No. 1.4e-12;  
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGGVKNNF-VPTNWGSKAF 30  
Db 1 THRLAGLSRSGGVKNNF-VPTNWGSKAF 29

RESULT 13  
US-07-794-288D-26  
Sequence 26, Application US/07794288D  
Patent No. 5580953  
GENERAL INFORMATION:  
APPLICANT: ELISABETH ALBRECHT,  
APPLICANT: HOWARD JONES,  
APPLICANT: LAURA S.L. GARETA,  
APPLICANT: KATHRYN S. PRICKETT and  
APPLICANT: KEVIN BEADOMONT  
TITLE OF INVENTION: NOVEL AMYLIN ANTAGONIST  
TITLE OF INVENTION: PEPTIDES AND USES THEREFOR  
NUMBER OF SEQUENCES: 227  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: First Interstate World  
STREET: Center  
STREET: 633 West Fifth Street,  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44  
MEDIUM TYPE: Mb storage  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: IBM M.S. DOS (Version  
5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/794,288D  
FILING DATE: Herewith  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/794,288  
FILING DATE: 19-NOV-91  
ATTORNEY/AGENT INFORMATION:  
NAME: Duft, Bradford, J.  
REGISTRATION NUMBER: 32,219  
REFERENCE/DOCKET NUMBER: 193/153  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:

LENGTH: 30 AMINO ACIDS  
TYPE: AMINO ACID  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PEPTIDE  
FEATURE:  
OTHER INFORMATION:  
US-07-794-288D-26

Query Match 85.7%; Score 128.5; DB 1; Length 30;  
Best Local Similarity 90.0%; Pred. No. 1.5e-12;  
Matches 27; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 1 THRLAGLSRSGGVKNNF-VPTNWGSKAF 30  
Db 2 THRLAGLSRSGGVKNNF-VPTNWGSKAF 30

RESULT 14  
US-08-460-890A-45  
Sequence 45, Application US/08460890A  
Patent No. 5994109  
GENERAL INFORMATION:  
APPLICANT: WOO, Savio L.C.  
APPLICANT: Smith, Louis C.  
APPLICANT: Cristiano, Richard J.  
APPLICANT: Gottchalk, Stephen  
TITLE OF INVENTION: NUCLEIC ACID TRANSPORTER SYSTEMS AND  
TITLE OF INVENTION: METHODS OF USE  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LYON & LYON  
STREET: 633 West Fifth Street  
STREET: Suite 4700  
CITY: Los Angeles  
STATE: California  
COUNTRY: U.S.A.  
ZIP: 90071-2066  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
MEDIUM TYPE: storage  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: IBM P.C. DOS 5.0  
SOFTWARE: FASTSEQ for Windows 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,890A  
FILING DATE: June 5, 1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/167,641  
FILING DATE: December 14, 1993  
APPLICATION NUMBER: 07/855,389  
FILING DATE: March 20, 1992  
APPLICATION NUMBER: PCT/US93/02725  
FILING DATE: March 19, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Warburg, Richard J.  
REGISTRATION NUMBER: 32,327  
REFERENCE/DOCKET NUMBER: 212/066  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (213) 489-1600  
TELEFAX: (213) 955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 45:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FEATURE:  
OTHER INFORMATION: "Xaa" stands for an unnatural amino  
acid with R group forming a ring  
OTHER INFORMATION: acid with R group forming a ring

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; OTHER INFORMATION: attached to "asp" in position 1
; OTHER INFORMATION: "Lys" in position 22 has an
; OTHER INFORMATION: n-x substitution.
US-08-460-890A-45

```

Query Match	85.7%;	Score 128.5;	DB 2;	Length 35;
Best Local Similarity	90.0%;	Pred. No. 1.8e-12;		
Matches 27; Conservative	2;	Mismatches 0;	Indels 1;	Gaps 1;

QY	1	THRLAGLLSRSGGMVKSNFVPTNVGSKAF	30
		: : :	
Db	7	THRLAGLLSRSGGVKNKF-VPTNVGSKAF	35

Query Match	85.7%;	Score 128.5;	DB 3;	Length 35;
Best Local Similarity	90.0%;	Pred. No. 1.8e-12;		
Matches 27; Conservative	2;	Mismatches 0;	Indels 1;	Gaps 1;

Search completed: August 26, 2002, 15:52:15  
Job time: 147 sec

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